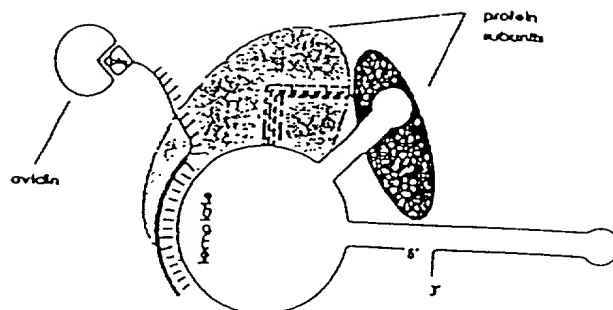


FIGURE 1

PANEL A



elution with
displacement of oligonucleotide

PANEL B

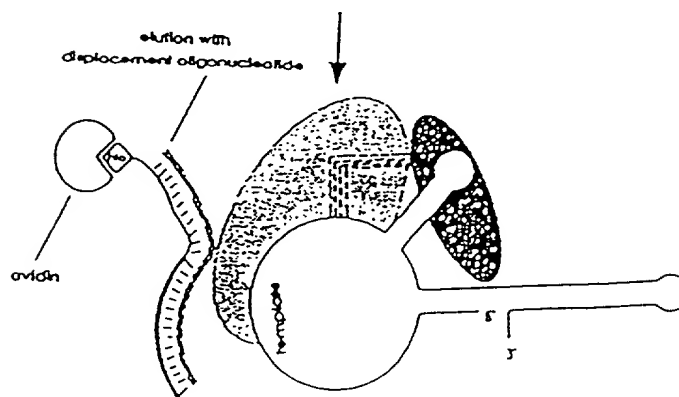


FIGURE 2

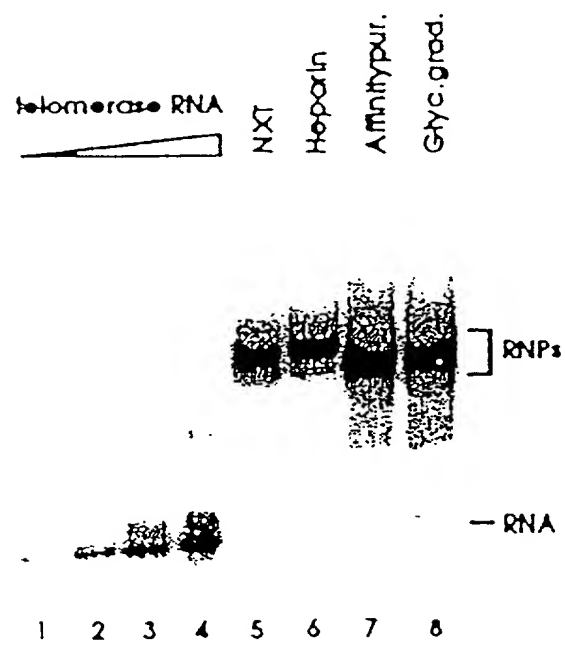


FIGURE 3

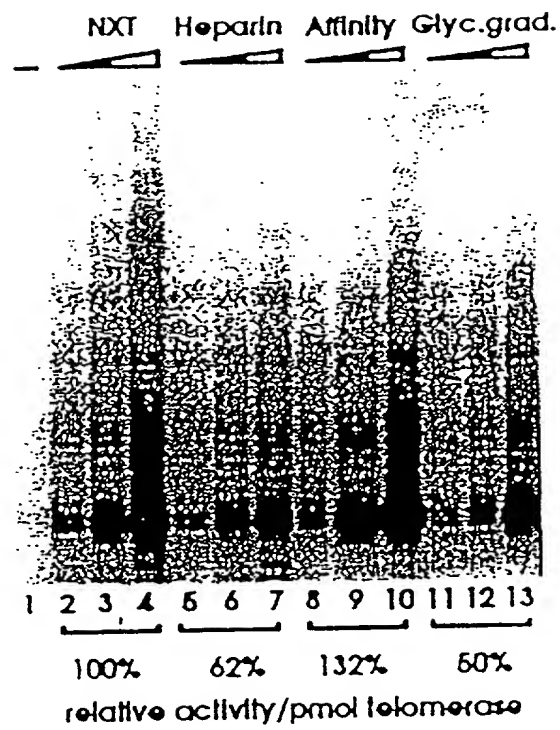


FIGURE 4

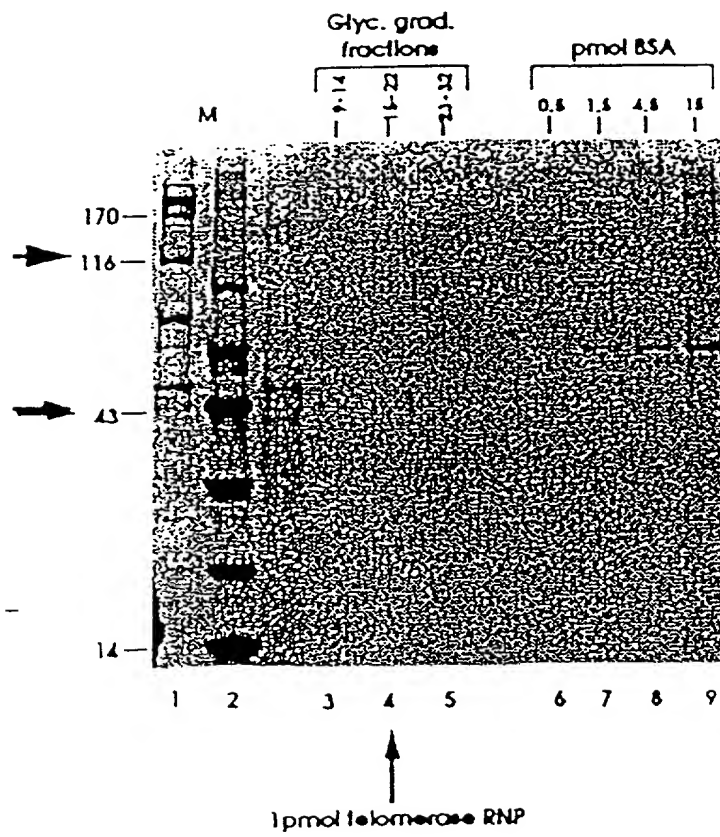


FIGURE 5

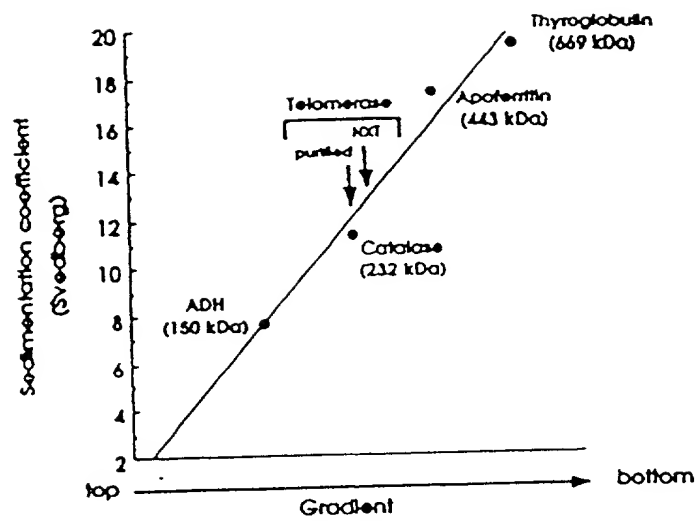


FIGURE 6

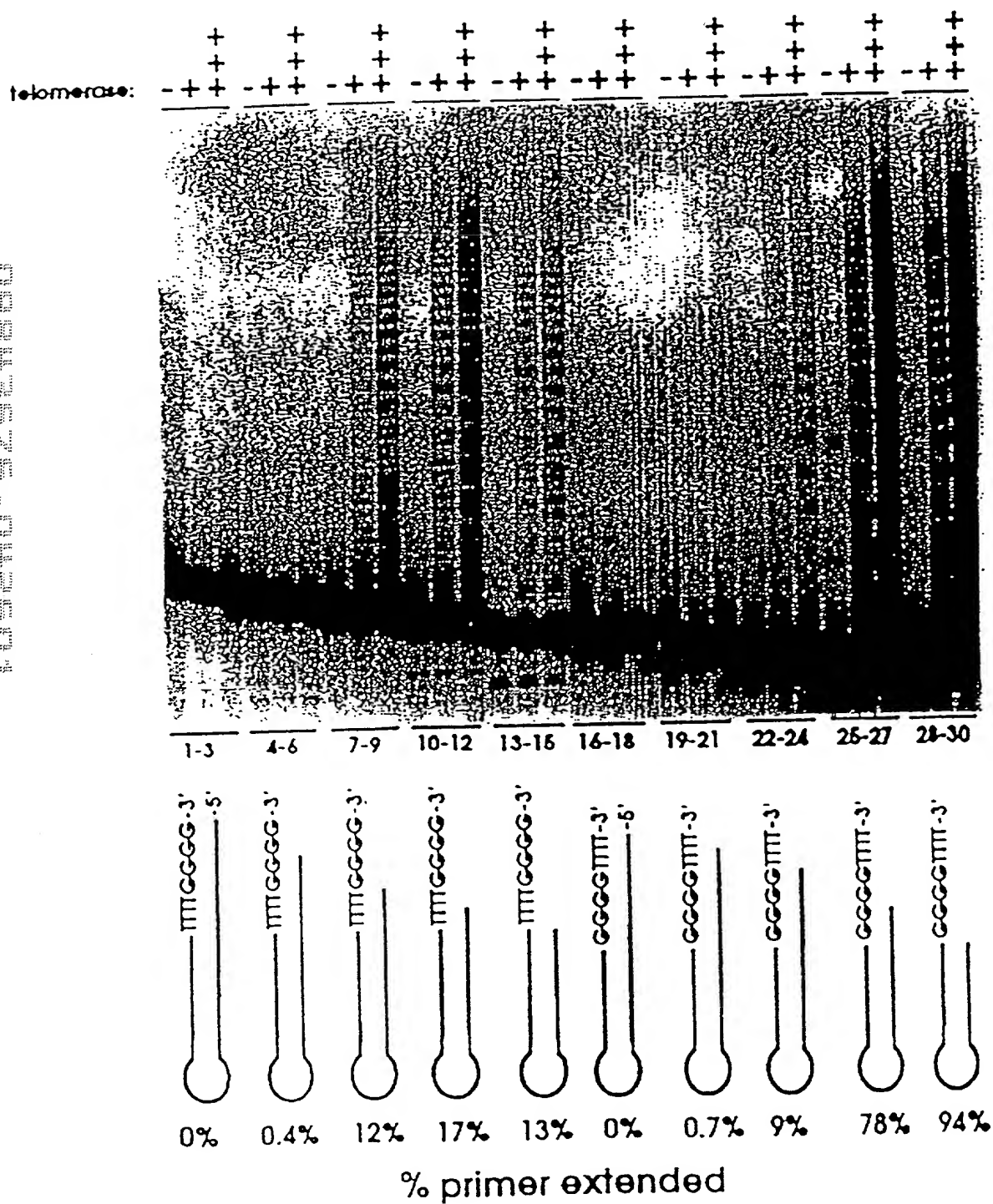


FIGURE 7

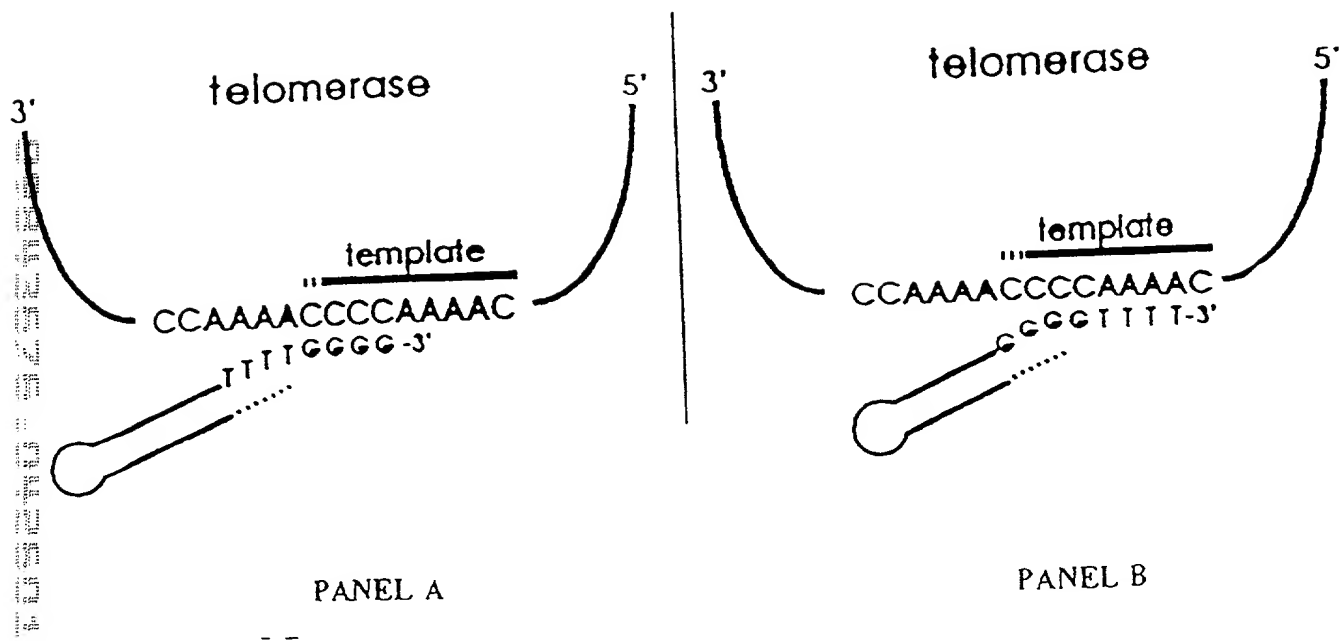


FIGURE 8

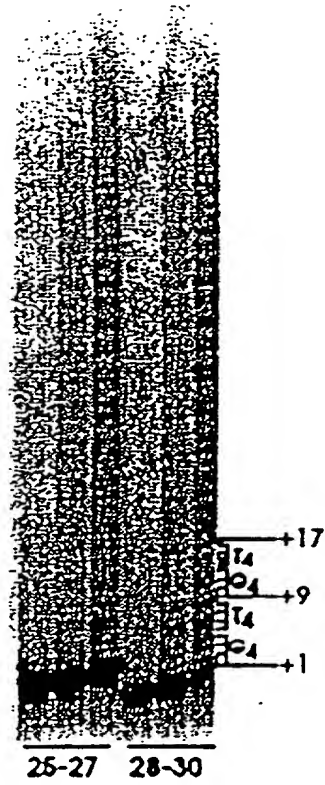


FIGURE 9

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251 TTAGAAGATA TTAATAATATT TGC GCAGACA AATATTGTTG CTACTCCACG
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTTCT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC A
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
 1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
 1051 TCCTCTTCCA GAAAATTGGC GGAACGGAA ACAAAAAATC GAAAACCTGA
 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
 1151 TACACAAC TG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA
 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
 1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTAC
 1301 AAAAATTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
 1351 GGTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
 1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
 1651 ACCGAAGAAA ACTACTTTC GTCCAATTAT GACTTTCAAT AAGAAGATTG
 1701 TAAATTCAGA CCGGAAGACT ACAAATTA CTACAAATAC GAAGTTATTG
 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
 1801 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
 1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA
 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAATATC
 1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
 2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
 2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
 2151 AACAAAATGA CTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
 2251 CCAATATAAT TACATTAAC TTAATGGGAA GTTTTATAAA CAAACAAAAG
 2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAACTT
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAACTACA
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAACTCT
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTTGTC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTGT TCTTATATAC
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNIRKRLK DKVIEKIAYM
301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELH
401 KNLLLEKINT REISWMQVET SAKHFYFDH ENIYVLWLL RWIFEDLVVS
451 LIRCFYVTE QOKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
501 EEWKKS LGFA PGKLR LIPKK TTFRPIMTFN KIVNSDRKT TKLTTNTKLL
551 NSHMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKT LIVEAKQ
701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFY
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVL FIEKL
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
851 SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
901 HYFRKTITTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID
951 LEVSKIIYSV TRAFFKYLCV NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001 KYIFNRVCM LKAKEAKLKS DQCQSLIQYD A

FIGURE 11

1 CCCCCAAACC CCAAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG
 51 GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTAA
 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT
 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCTG
 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651 TTGAGACAAT TGAAAAAGCT GTTTACAACCT GAAGGAATCG CAGTTCTGAA
 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
 801 TAATGGAATA TACGTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951 AAAAGAAGCA GCGGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
 1001 TTGTTGATTG TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
 1051 AAAGAAGAAG AGCTATCACA ATCCTGATTG TTAAAGATTT CAAAAATTCC
 1101 AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATT
 1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
 1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
 1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
 1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
 1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
 1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
 1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA
 1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
 1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
 1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
 1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
 1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
 1751 GGGGTTTTGG GG

FIGURE 12

1 ----- 60
 CCCCCAAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAATTGAGGTAGTTAGA
 GGGGTTTGGGGTTTGGGGTTTGGGGATATTTTCTTTTAACTCCATCAAATCT
 a P Q N P K T P K P L * K K K K L R * F R -
 b P K T P K P Q N P Y K K R K N C G S L E -
 c P K P Q N P K T P I K K E K I E V V * K -
 AATAAAATATTATCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT
 61 ----- 120
 TTATTTTATAATAAGGGCGTGTACCTCTACCTATAACTAAACCTACTATATCTTTTAA
 a N K I L F P H K W R W I L I W M I * K I -
 b I K Y Y S R T N G D G Y C F G C Y R K F -
 c * N I I P A Q M E M D I D L D D I E N L -
 TACTTCTCAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
 121 ----- 180
 ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAACATCACTGTTCTTCTACGTTTT
 a Y F L I H S T S I A A L V V T R K D A K -
 b T S * Y I Q Q V * Q L L * * Q E R M Q N -
 c L P N T F N K Y S S S C S D K K G C K T -
 CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
 181 ----- 240
 GTAACCTTAGACCGAGCTTTAGCGGAAGTAAGTATAAGGTTTCAACGTTTTGTTAATC
 a H C N L A R N R L H C L F Q S C K N N * -
 b I E I W L E I A F I D Y S K V A K T I R -
 c L K S G S K S P S L T I P K L Q K Q L E -
 AGTTCTACTTCTCGGATGCAAACTTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
 241 ----- 300
 TCAAGATGAAGAGCCTACGTTTAGAATATTGCTAAGAAAGAACTCTTTAATCAAAATT
 a S S T S R M Q I F I T I L S C E N * F * -
 b V L L L G C K S L * R F F L E K I S F K -
 c F Y F S D A N L Y N D S F L R K L V L K -
 AAAGCGGAGAGCAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
 301 ----- 360
 TTTCCGCTCTCGTTTCTCATCTTAACTTTGTAATGATTACAAATTTATTTAGTCCATT
 a K A E S K E * K L K H Y * C L N K I R * -
 b K R R A K S R N C N I T N V * I K S G N -
 c S G E Q R V E I E T L L M F K * N Q V M -
 TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATCGAGAAAATTACTTAA
 361 ----- 420
 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTAATGAATT
 a C G L F Y F L D H F L R S I M E K I T * -
 b E D Y S I F * I T S * G A L W R K L L N -
 c R I I L F F R S L L K E H Y G E N Y L I -
 TACTAAAAGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAATTT
 421 ----- 480
 ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA
 a Y * K V N S L D Y F P S Q Q C C V Y * i -
 b T K R * T V W I I S L A N N D E Y I K F -
 c L K G K Q F G L F P * P T M M S I L N S -

FIGURE 12 (cont.)

CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
 481 ----- 540
 GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA
 a H M R M S Q R I S I H O T Y Q R Q T R Y -
 b I C E C V K G S R Y I R L T K D K L A I -
 c Y E N E S K D L D T S D L P K T N S L -
 AAAACCGAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATGCAATTTACTATTTCG
 541 ----- 600
 TTTTCGGTTCTTTTCAAACCTATTAGCTTGTCTGCTTCTTGAATAACGTAATGATAAGC
 a K T Q E K V C * S N S R R T Y C I Y Y S -
 b K R K K K F D N R T A E E L I A F T I R -
 c N A R K S L I I E Q Q K N L L H L L F V -
 TATGGGTTTTATTACAATTGTTTATAGGTATCGACGGTGAACCTCCCGAGTCTTGAGACAAT
 601 ----- 660
 ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA
 a Y G F Y Y N C F R Y R R C T P E S C D N -
 b M G F I T I V L G I D G E L P S L E T I -
 c W V L L Q L F * V S T V N S R V L R Q L -
 TCAAAAAGCTGTTTACAACGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
 661 ----- 720
 ACTTTTTGACAAAATGTTGACTTCCCTAGCGTCAAGACTTTCAGACTACACATACGGTA
 a C K S C L Q L K E S Q F C K F * C V C H -
 b E K A V Y N C R S S E S S D V Y A I -
 c K K L F T T E G I A V L K V L M C M P L -
 TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
 721 ----- 780
 ATAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT
 a Y F V N * S Q I S Y L N L M D S Y R N K -
 b I L C I N L K Y L I S I * W I A I E T N -
 c F C E L I S N I L S Q F N G * L * K Q T -
 CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
 781 ----- 840
 GGTTTATTTGCTACGTTCAAATTACCTTATATGCAATTTAGGAAACCTGTTTACGTGTG
 a P N K P C K F N G I Y V K S F G T N A H -
 b Q I N H A S L M E Y T L N P L G Q M H T -
 c K * T * Q V * W N I R * I L W D K C T L -
 TGAATTTATATTGGATTCTTAAAGCATAGATACAGAATGCTTTAGAGACTGATTTAGC
 841 ----- 900
 ACTTAATATAACCTAAGCAATTTCGTATCTATGTCTTACGAAATCTCTGACTAAATCG
 a C : Y I G F * K H R Y T E C F R D C F S -
 b E F I * D S * S I D T Q N A L E T D * L A -
 c N L Y A * L * S A * I H R M L * R L I * L -
 TTACAACAGATTACCTGTTTGGATTACTCTTGCTCATCTCTTATATCTTTAAAGAAGCA
 901 ----- 960
 AATGTTGCTCTAATCGACAAAACCTAATGAGAACGAGTAGAGAATATAGAAATTTCTTCGT
 a L Q Q I T C F D Y S C S S L I S L K E A -
 b Y N R L P V L I T L A H L L Y L * K K Q -
 c T T D Y L F C L L L L I S Y I F K R S R -
 GGCGAAATGAAAGAAGACTAAAGAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
 961 ----- 1020
 CCGCTTACTTTCTTCTGATTTCTTTCTTAAAGTTTAAACAACCTAAGAAGACATTGG
 a G E M K R R L K K E I S K F V D S S V T -
 b A X C K E D * R K R F Q N L L I L L * P -
 c R N E K K T K E R D F K I C C F F C N R -
 GGAATTAACAACAAGAAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTCT
 1021 ----- 1080
 CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTCTCGATAGTGTAGGACTAAG
 a G I N N K N : S N E K E E E L S O S C F -
 b E L T T R I L A T K K K K S Y H N P D S -
 c N * Q Q E Y * Q P K R R R A I T I L I L -

FIGURE 12 (cont.)

1081 TTAAGATTTCAAAAATCCAGGTAAGAGAGATACATTCAATTAATTCATATATTATAG 1140
AATTTCTAAAGTTTTAAGGTCCTTCTCTATCTAAGTAATTTAAGTATATAATATC

a L K I S K I P G K R D T F I K I H I L -
b * R F Q K F Q V R E I H S L K F I Y Y S -
c K D F K N S R * E R Y I H * N S Y I I V -

1141 TTTTTCATTTACAGCTGTTATTTTCTTTTATCTTAACAATATTTTGTAGCTGGAA 1200
AAAAAGTAAAGTGTGACAATAAAGAAAATAGAATTGTTATAAAAACTAATCGACCTT

a F F I S Q L L F S F I L T I F F D * L E -
b F S F H S C Y F L L S * Q Y F L I S W K -
c F H F T A V I F F Y L N N I F C L A G S -

1201 GTAAAAAGTATCAAAATAAGAGAAGCGCTAGACTGAGGTAAGTCTTATTCACATTCAT 1260
CATTTTTCATAGTTATTTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a V K S I K * E K R * T E V T * L I H I H -
b * K V S N K R S A R L R * L S L F T F I -
c K K Y Q I R E A L D C G N L A Y S H S -

1261 AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA 1320
TCTAGCTGGAAGTATATAGGTATGCTACTATTCTTGTGCTCAGTAGGCAAAATTTT

a R S T F I Y P I R C * G N S S H P F * K -
b D R P S Y I Q Y D D K E T A V I R F K N -
c I D L H I S N T M I R K Q Q S S V L K I -

1321 TAGTGCTATGAGGACTAAATTTTATAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA 1380
ATCAGGATACTCTGATTTAAAAATCTCAGTCTTTACCTCGGCTTTAGAATTAGTTTTT

a * C Y E D * I F R V K K W S R N L N Q K -
b S A M R T K F L E S R N G A E I L I K K -
c V L C G L N F * S Q E H E P K S * S K R -

1381 GAATGCGTCGATATTGCAAAAAGAAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA 1440
CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTAGAAAGCAATTATTCATAATGGT

a E L R R Y C K R I E L * I F R * V L P -
b N C V D I A K E S N S K S F V N K Y Y Q -
c I A S : L Q K N R T L N L S L I S I T N -

1441 ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAGAAATAAA 1500
TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGCTTCTAGTAATTTCTTTATTT

a I L I D C R D * R G N C T E D H * R N K -
b S C L I E E I D E A T A Q K I I K E I K -
c L D C L K R L T R Q L H R R S L K K * S -

1501 GTAACCTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA 1560
CATTGAAAATAATTAATCTCTTATTGATTAAATGATTATATCTCTAGTCGCTAGAAGTT

a V T F I N * R I N * I T N I E I S D L Q -
b * L L L I R E * T K L L I * R S A I F N -
c N F Y * L E N K L N Y * Y R D Q R S S I -

1561 TTGACGAAATAAAAGCTGAAGTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT 1620
AACTGCTTTATTTTCGACTTGATTCAATCTGTTATTTTATGTTTGAACCAGTTT

a L T K * K L N * S * T I K N T N L G Q N -
b C R N K S C T K V R Q * K I Q T L V K I -
c D E I X A E L K L D N K K Y K P W S K Y -

1621 ATTGAGGAAGGAAAAGAAGACCAAGTTAGCAAAAAGAAAAATAAGCCAATAAATAAATGA 1680
TAACTCCTTCTCTTCTCTGGTCAATCGTTTCTTTTATTTCGTTATTTATTTTACT

a I E E G K E D Q L A K E K I R Q * I K C -
b L R K E K K T S * Q K K K * G N K * N E -
c C G R X R R P V S K R K N K A I N K M S -

FIGURE 12 (cont.)

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      GTACAGAAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT
1681 ----- 1740
      CATGTCCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCCAA

a      V  Q  K  C  R  N  K  R  F  I  F  F  N  N  L  L  K  R  G  V  -
b      Y  R  S  E  E  I  K  D  L  F  F  S  I  I  Y  C  K  E  G  F  -
c      T  E  V  K  K  *  K  I  Y  F  F  Q  *  F  I  E  K  R  G  F  -

      TTGGGGTTTTTGGGGTTTTTGGGG
1741 ----- 1762
      AACCCCAAACCCCAAACCC

a      L  G  F  W  G  F  G  -
b      W  G  F  G  V  L  G  -
c      G  V  L  G  F  W  -
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FIGURE 13

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2 EVDYQAOADNHGIIHSALKTCEEIKCAKTLYSWQKVIQVIRCRNOSQSHYKDL 51
19 ELELEMOENQNDIQVRVK . IDDPKQY . LVNVTAACLLQEGSSYODK 62
52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF . STGLMIELIDKCLVELL 100
63 DERRAITKALL . EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF . 107
101 SSSDSDRQKLQCFGFQKGNQLAKXTHLLTALSTQKQYFFQDEWNQVRAM 150
108 . . . . . CVVHKNTOPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144
151 IGNELFHRHLYTKYLI FORTSEGTLVQFCGNVVDHLKVNDKFDKKQKGA 200
145 FDATEFKNLY . . . . . LDRILSQDIRKELTRFKCLQRCVRSKF 181
201 ADME PRCCSTCKYNVKNKDHFLNNINVPNNNMKSRTRIFYCTHF 247
182 SEFNEYQLGKYCTES . QRKKTMFRLSVTNKQKWDQTKKK . 220
248 NRNNQFFKKHEFVSNKNNISAMDRAQITFTNIFRNRIRKKLKDKVIEKI 297
221 . RKENLLTKLQAIKESDKSKRETG . . . . . DIMNVEDAIALKAPVAMKKI 264
298 AYMLEKVKDFNFNYLLTKSCLPENWRERKQKIENLINKTREESKYEE 347
265 AKRQAMK . . . . . KHMKAPKIPNSTLESKYLTFKD 294
348 LFSYTTDNKCVTFINEFFYNILPKDFLTGRNRKNFQKKVKYVELNKHE 397
295 LIKFCHISEP . . . . . KERVYKILGKKYPTEEEYKAAFQDSASAPFN . PE 338
398 LIHKNLLEKINTREISWMQVETSAKHFFYFDHENIYVLWKLRLWIFEDL 447
339 LAGKRMKIEISKTWENELSAKGNTAEVWNLISSNQLPYMAHLRNLNS . 386
448 VVSLRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE 497
387 . . . . . ILKAGVSD . . . . . 394
498 KEVEEWKKSGLGAPGKRLRLIPKKTFRPIMTFNKKIVNSDRKTKLTNT 547
395 . . . . . TTSS 398
548 KLLNSHMLMLTKLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGPKL 597
399 IVINK . . . . . ICEPKAVENSKM 415
598 FFATMDIEKCYDSVNREKLTSTFLKTKLLSSDFWIMTAQILKRKNIVID 647
416 F . . . . . PLOFFSAIEAVN . EAVTKGFRAK . . . . . RENMNLKGQIEAVKE . VVE 457
648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKT LIVE 697
458 KTDEEKKDM . . . . . ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496
698 AKQRNYFKKDNLLQPVINICQYNYINFNGKIFYKQTKGIPQGLCVSSILSS 747
497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMGGAKKYGSVRTCECALVLGL 546
748 FYYATLEESSGLFLRDESMNPENPNVLLMRLTDDYLLITTQENNAVLFI 797
547 MVKQRCXSSFYIFSSPSSQCNCYLEVDL . . . . . 576
798 EKLINVSRENGFKFNMKK . LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
577 . . . . . PGDEL RPSMQKLQEKGLGG . . . . . TDFPYECIDEWTKNKT HVD 617
847 WIGISIDMKTALMPNINLRIEIGILCTNLNMQTKKASMWLKKKLKSFLM 896
618 NIVILSDMMIAEGYS DINVRGSSIVNSI . . . . . KKYKDEVN 653
897 NNITHYFRKTITTFDFANKTLNKLFISSGKYMQCAKEYKD . HFKNLAM 945
654 PNIXIF . . . . . AVDLEGY . . . . . KCLNLGDEFENNYIKIFGM 687
946 SSMIDLEVSKIISVTRAFFKYLVCNIKDTIFGEEHYPOFFLSTLKHPIE 995
688 SDSI . . . . . LKFISAKQGA . . . . . NMVE 706
996 IFSTKKYIFNRVC 1008
707 VI . . . . . KNFALQKIG 717

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FIGURE 14

132 LSTQKQYFFQDEWNOVRAMIGNEL.FRHLYTKYLIFORTSE..GTLVQFC 178
 1 MSRRNQ.KKPQAPIGNETNLDVFLQNLVYKQIEHYKTQQQI 43
 179 GNNVFDHLKVNDKFDKKQKGAADHNEPRCCSTCKYNNVKNKDHFLNNIN 228
 44 KEEDLKKLKFKNQDQDGNNGDDDEE.NNSNKQOELLRRVN 84
 229 VPNNWNHKSRTIRFYCTHFNRMNQFFKHEFVSNNKNNISAMDRAQTIFTN 278
 85QIKQOVQLIKK.VGSKEVDLNLNEDENKKN 114
 279 IFRFNRIKKLKDVKIEKIAYMLEKVDFNFNYLTSCPLPENWRERKQ 328
 115 GLSEQOVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRETDTY 164
 329 KIENLINKTREEKSKYEEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
 165 DTEKWFEISHQKNYVSIYANQKTSYCWMLKDYFNK 200
 378 RNRKNFQKKVKKYVELNKHLEIHKNLLEKINTREISWMOVETSAKHFFY 427
 201 NNYDHLNVSINRLE. TEAEFYAFDDFSQTIKLTNNSYQTVNID. 242
 428 FDHENIYVLWKLRLWI. FEDLVVSLIRCFYFVTEQQSKYSKTYYYRKN 475
 243 VNFNNLCILALLRFLLSLERFNILNIRSSY. TRNQYNFEKIGELLETI 290
 476 WDVIMKMSIADLKKETLAEOEKEVEEWKSKLGFAPGKRLRIPKKTFRP 525
 291 FAVVFSHRHLQGIHLQVPCFAFYLVNSSQISVXDSLO 330
 526 IMTFNKKIVNSDRKTTKLTNTKLLNSHLMLKTLKNRMFKDPFGFAVFN 575
 331 VVSFSTDLKLV. TNKVQDYFKFLQEFPRLTHVSQAIPVSATNAVENL 378
 576 DDVMKKYEEFVCKWKVQVQPKLF.FATMDIEKCYDS. VNREK 615
 379 NVLLKKVKHANLNLVSIPTQFNDFYFVNLOHLKLEFGLPNILTKQK 426
 516 LSTFLKTTKLLSSDFWIMTAQILKRNKIVIDSKNFRKKEMK 657
 427 LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNO 476
 558 DYFRQKFOKIALEGGQYPTLFSVLEN EQNDLNAKKT LIVEAKQRNYFK 705
 477 EETPETKDETPESTSGMKFFDHLSELTELEDFSVNLQATQEIY 520
 706 KDNELQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEE 755
 521 .DSLHKLIRSTNLKKFKLSYKYEKSKMDTFIDLKNI.YETLNN 564
 756 SSLGFLRDESKNPNPNVNLMLRLTDDYLLITTOENNAVLFIKLINVR 805
 565LKRCVNI SNPHGNISYELTNKDSTFYKFKLTLNQE 600
 806 ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK 855
 601 LQHAKYTFK QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ 648
 856 TLALMPNINLRIEGILCTNLNMOTKKASHWLK.KLKSFLMNNITH 901
 649 NVNI.IASLLYPNNIQKNPKNPKNLLFFKQFEQLKNLENVINC 691
 902 YFRKTITTEDFANKTLNKLFISSGKYHQAKEYKDHFKKNLAMSS 948
 692 ILDOHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFTLQQLPEL 741
 949 IDLEVSKIIYSVTRAFFKYLVCNKIDT. IFGEEHY 982
 742 NQVYINQOELTVSEVHKQVWENHKQAFYEPLCEFIKESSTLQIDF 791
 983 POFELSTLKHPIEFSTKKY IFNRVCMILKAKEAKLKSQCSLIQ 1028
 792 QONTVSDDSIKKILESISESKYHHYLRNPSQSSSLIKSENEEIQELLK 840

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[illegible]

FIGURE 16

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1 MEMDIDLDDIENL . LPNTFNKYSSSCSDKKGCKTLKSGSKSPS. 42
  | | | | | | | | | | | | | | | | | | | | | |
491 IELAIAVKNLDEIKGHTAIFSDVSGSHSTSHSGGAKXYGSRVTCLEC 540
  | | | | | | | | | | | | | | | | | | | | | |
43 LTIPKLQKQ . LEFYFSDANLYNDSFLRKLVLKSQEORVEIETLL 85
  | | | | | | | | | | | | | | | | | | | | | |
541 ALVLGLMVKQRCCKSSFYIFSSPSSQCNCYL . EVDLPGDELRPMSMQKLL 589
  | | | | | | | | | | | | | | | | | | | | | |

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MEMDIDLDDIENL . LPNTFNKYSSSCSDKKGCKTLKSGSKSPS. 42

FIGURE 17

| | Motif A | Motif B |
|--------------------|---|-----------------------|
| Consensus | h--h <h>h</h> h--h--h | h---+ QC ---Sp |
| telomerase p123 | GQPKLFPATMDIEKCYDSVNREKLSFLKTTKLL-100-KFYKQTKGIP QC LCVSSILSSFFYYATLEESSLGFL | |
| Dong (LINE) | KNRNLHCTYIDYKKAFDSIPHSWLIOVLEIYKIN-28-RQLAIKKGIY QC DSLSPJWFCALNPLSHQLHNDR | |
| al S.c. (group II) | FGGSNWFEV DL KKCFDTISHDLIIKELKRYISD-26-HVPVGPVVCV QC APTSPALCNAVLRRLDRRLAGLA | |
| HIV-RT | LKKKKSVTVL DL VGDAYFSVPLDEDFKRYTAFTIP-7-GIRYQYNVLR QC WKGS SP AI FC SSMTKIL EP FRKQN | |
| L8543.12 | VLPELYFMK FL VKSCYDSIPRMECMRILKDALKN-68-KCYIREDDGL FC ESSLS SA ?IVDLVYDDLL LE FYSEPK | |
| | | |
| Consensus | h--Yh DD h <h>h</h> | |
| telomerase p123 | -14-LMRLTDDYLLITTTQENN-0-AVLFI E KLINVSREN CF KYN TR KLQT-23-QDYCDWIGIS I | h-h LC h-h |
| Dong (LINE) | -16-HLIYMD DI KLYAKNDKE-0-MKKLIDTTTIFSN DIS MQFGL DR CKT-25-KCJYKYL GF QQ | |
| al S.c. (group II) | -55-YVRYAD DI LIGVLGSKN-2-KIIKRD LNN FLNS I L GL TINE ER TL I -4-ETPAR FL G YNI | |
| HIV-RT | -4-IYQYMD DL YVGSHLEIG-1-HRTK IE ELRQHLLR WGL TT PD FR HQK -0-EP FL WM GYEL | |
| L8543.12 | -8-ILKLAD DF LIISTDQQQ...VINIKKLAM CF QKYN AR ANR-41-IRSKSSK GIFR | |
| | | |
| | Motif D | Motif E |
| | Ch-h--- K | h-h LC h-h |

FIGURE 18

| | |
|----------------|---|
| telomerase p43 | LQKQLEFYEYSDANLYNDSEFLRKLVLKSGEQRVEIETLLM |
| human La | ICHQCEYYEGDENLPRDKFLKEQI.KLDEGWVPLEIMIK |
| Xenopus LaA | ICEQCEYYEGDENLPRDKFLKQOI.LLDDGWVPLETMIK |
| Drosophila La | ILRQVEYYEGDANLNRDKFLREQIGKNEDGWVPLSVLVT |
| S. c. Lhplp | CLKQMEFYSEFNFPYDRFLRTTAEK.NDGWVPISTIAT |

FIGURE 19

1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
 61 tagatttaatt itagaaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagt agggtaaga ttgacgatcc taagcaatat ctctgaacg tcaactgcagc
 241 atgtttgtg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt ctgaggtgg ctgagctga tctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgttgtt
 421 ccacaagaat actcaacat tcacgaaaa gtacttcaac aaagcagtac tttgcctaa
 481 tgacttactg gaagtctgtg aatttgata ggttctctat attttgatg caactgaatt
 541 caaaaatttg tatctgata ggatacttc ataagatatt cgtaaggaac tcactttccg
 601 taagtgtta caaagatgag tcagaagcaa gtttctgaa ttcaacgaat actaacttg
 661 taagtattgc actgaatcct aacgaagaa aacaatgttc cgttacctct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggcttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcttaactct accttggat caaagtactt
 961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
 1021 gatccttgg taaaaatacc ctaagaccga agaggaaatc aaagcagcct ttggtgatc
 1081 tgcactgca ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
 1141 aacatgggaa atgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaatt
 1201 ttcaagcaat taactccat atatggccat gttacgtaac ttgtctaaca tctaaaagc
 1261 cgggtttca gatactacac actctatgt gatcaacaag atttgtagc ccaaggccgt
 1321 tgagaactcc aagatgtcc ctctcaatt ctttagtgc attgaagctg ttaatgaagc
 1381 agttactaag gaattcaagg ccaagaagag agaaaatag aatcttaag gtcaaatcga
 1441 agcagtaag gaagtgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
 1501 aaccgaagaa ggagaattg ttaagtcaa cgaaggaatt ggcaagcaat acattaactc
 1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaatca-aaggacacac
 1621 tgcaatcttc tctgatgtt ctggttctat gactacctca atgtcaggtg gagccaagaa
 1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaata
 1741 acgttgtaa aagtcctcat tctacatct cagttcacct agttctcaat gcaataagt
 1801 ttacttagaa gtgatctcc ctggagacga actccgtcct tctatgtaa aactttgca
 1861 agagaaagga aaacttggtg gtgtactga ttcccctat gagtgcattg atgaatggac
 1921 aaagaataaa actcacgtag acaatctgt tattttgtct gatagatga ttgcagaagg
 1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
 2041 tgaagtaaat ctaacatta aaactttgc agttgactta gaaggttacg gaaagtgcct
 2101 taatctaggt gatgagtca atgaaaacaa ctacatcaag atattcggtg tgagcgattc
 2161 aatcttaag ttacttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
 2221 cttgccctt caaaaaatag gacaaaagt agtttctga gattcttcta taacaaaaat
 2281 ctacccccac tttttgtt tattgcatag ccattatgaa atttaatta ttatctatt
 2341 atttaagta ctacatagt ttatgtatc cagtctatta gccattcaa atgattctgc
 2401 aaagaacaaa aaagattaaa a

FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN
YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMTFRYLSVTNKQKWDQTK
KKRKENLLTKLQAIKESDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK
APKIPNSTLESKYLTFKDLIKFCHISEPKEVYKILGKKYPKTEEEYKAAFGDSASAP
FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNKLGQIE
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG
HTAIFSDVSGSMSTMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ
CNKCYLEVLDLPGDEL RPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHTVDNIVILSD
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGYGKCLNLGDEFNENNYI
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

FIGURE 21

1 tcaatactat taattaataa ataaaaaaaa gcaactaca aagaaatgt caaggcgtaa
 61 ctaaaaaag ccataggctc ctataggcaa tgaacaaat ctgtatttg tattacaaa
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgatgat gaagaaaaca actcaataa ataataaga ttattaagga gagtcaatta
 301 gattaagtag caagttaat tgataaaaa agttggttct aaggtagaga aagatttgaa
 361 ttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aatagggtta gtattaaat ttagtattta acatggacta
 481 ccagttagat ttaaatgaga gtgggggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggtttgaat tatctcatga ccaaaaaat tatgtatcaa ttacgccaa
 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca
 661 tcttaagtga agcattaaca gactagaac tgaagccgaa ttctatgctt ttgatgattt
 721 ttcacaaaca atcaaaacta ctaataatc ttactagact gtaacatag acgttaattt
 781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa
 841 tattttgaat ataagatctt cttatacaag aaattaatat aatttgaga aaattgggtga
 901 gctacttgaa actactctcg cagttgtctt ttctcatcgc cactacaag gcattcattt
 961 acaagttcct tgcgaagcgt tctaatttt agttaactcc tcatcataaa ttacggttaa
 1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaaca
 1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
 1141 ggctatccca gttagtcta ctaacgctgt agagaacctc aatgtttac ttaaaaagg
 1201 caagcatgct aatcttaatt tagttctat ccttacctaa ttcaattttg atttctactt
 1261 tgttaattta taacatttga aattagagt ttgattagaa ccaaatattt tgacaaaaca
 1321 aaagcttgaa aatctacttt tgagtataa ataataaaaa aatcttaaat tttaagatt
 1381 aaacttttac acctacgttg cttagaacac ctccagaaaa cagatattaa aacaagctac
 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa cttaagatga
 1501 aactccaagc gaaagcaca gtggtatgaa atttttgat catctttctg aattaaccga
 1561 gcttgaagat ttacgctga acttgaagc tacccaagaa atttatgata gcttgcaca
 1621 acttttgatt agatcaaca atttaagaa gtcaaatga agttacaaat atgaatgga
 1681 aaagagttaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
 1741 taaaagatgc tctgtaata tatcaaatcc tcatggaac atttctatg aactgacaaa
 1801 taaagattct actttttata aatttaagct gacctaaac taagaattat aacacgctaa
 1861 gtatacttt aagtagaacg aatttaatt taataacgtt aaaagtgc aaattgaatc
 1921 ttctcatta gaaagcttag aagatattga tagtctttgc aaatctattg ctcttgtaa
 1981 aaatttaca aatgtaata ttatgccag ttgtctctat cccaacaata tttagaaaa
 2041 tctttcaat aagcccaatc ttctatttt caagcaattt gaataattga aaaatttgg
 2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
 2161 agaaaagaat aaaaaataa aagcattcat ttgaaaaga tatttttat tacaatatta
 2221 tcttgattat actaaattat taaaacact tcaatagtt cctgaattaa attaaattta
 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaagaat catcctaaac
 2401 ccttagctat atagattttg accaaaacac tgtaagtgtat gactctatta aaaagatttt
 2461 agaattcata tctgagtcta agtatcatca ttatttgaga ttgaacctta gttaatctag
 2521 cagtttaatt aaatctgaaa acgaagaat ttaagaactt ctcaagctt gcgacgaaaa
 2581 aggtgtttta gtaaaagcat actataaatt cctctatgt ttaccaactg gtacttatta
 2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaataaa tattaaatat
 2701 tgaatatttc ttgtctatt attgaataa tacatacaat agtcattttt agtgttttga
 2761 atatatttta gttatttaatt tcatttttt aagtaataa ttattttca atcattttt
 2821 aaaaaatcg

FIGURE 22

MSRRNQKKPQAPIGNETNLDVFLQNLEVYKSQIEHYKTQQQIK
EEDLKLLKFKNQDQDGNNGNDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK
DLNLNEDENKKNGLSEQQVKEEQRLTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR
ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNDHLNVSINRLETEAE
FYAFDDFSQTIKLTNNSYQTVNIDVNFNNLCILALLRFLSLERFNILNIRSSYTRN
QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF
STDCLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL
VSIPTQFNDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED
FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK
RCSVNISNPHGNISYELTNKDSTFYKFCLTNQELQHAKYTFKQNEFQFNNVKSAKIE
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNNLFFKQFEQLK
NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFKTLQQLPE
LNQVYINQQLLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSTLQLIDFDQNTVSD
DSIKKILESISESKYHHYLRNLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP
LCLPTGTYYDYNSDRW

FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKC GFHNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCHYLLTGELYNNVLTFGYKIARNEDVNNSLFC HS
ANVNVTLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK
WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNNSSSFFPYSKILPSSSSIKKLTDLR
EAIFPTNLVKIPQRLKVRJNLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDSLHLSR
QSPKERVLFHIVILQKLLPQEMFGSKKNKGKIIKNLNL LLSLPLNGYLPFDSLLKKL
RLKDFRWLFISDIWFTKHN FENLNQLAICFISWLF RQLIPKIIQTFFYCTEISSTVTI
VYFRHDTWKNLITPFIVEYFKTYLVENNVCRNHNSYTL SNFNHSKMRIIPKKS NNEFR
IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE
FKQRLKKFNNVLPELYFMKF DVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN
TNTGVLKLFNVVNASRVKPYELYIDNVRTVHLSNQDVINVVEME IFKTALWVEDKCY
IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV
INIKKLAMGGFQKYNAKANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF
KDLSINVTQNMQFHSFLQRH IEMTVSGCPITKCDPLIEYEV RFTILNGFLESLSNTS
KFKDNIILLRKEIQHLQAYIYIYIHIVN

FIGURE 24

| | |
|------------------|--|
| <i>Oxytricha</i> | LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT |
| <i>Euplotes</i> | LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT |

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIGURE 25

Motif 0

| | |
|-------|---|
| human | AKFLHWLMSVYVVELLRSPFFYVTETTFQKNR |
| tez1 | ISZIEWLVLGKRSNAXMCLSDFEKRRQIFAEFIYWLNSFIIPILQSFFYITESSDLNR |
| EST2 | LKDFRWLFISD---IWFTKHNFNENLNQLAICFISWLPRQLIPKIIQTFFYCTEISSTVT- |
| p123 | TREISWMQVET-SAKHPYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK |

. *.*** **

Motif 1

| | |
|-------|--|
| human | LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL |
| tez1 | TVYFRKDIWKLLCRPFI-TSMKMEAFKINENNVRMDTQK-TTLPPAVIRLLPKK--NTF |
| EST2 | IVYFRHDTWNKLITPFIVEYFKTYLVENWVCRNHNSYTLS--MFNHSKMRIIPKKSNEF |
| p123 | TYYYRKNIDVINKMST-ADLKKETLAEVQEKEVEEWKKS-LQFAPGKLRLIPKK--TTF |

..*. * . * * . * .**

Motif 2

| | |
|-------|--|
| human | RPIVNMDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA |
| tez1 | RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYHKLLTF |
| EST2 | RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF |
| p123 | RPIMTFNKKIVNSDRKTTKLTNTKLLNSHMLKTLKN-RMFKDPPGFAVFNHYDDVMKKY |

* * * *

Motif 3 (A)

| | |
|------|--|
| tez1 | KKDLLKHRMFOR-KXYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEPVIRKYATIHATS |
| EST2 | KQRLKKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFN |
| p123 | EEFVCKWKQVQPKLPFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRN |

. * . * * * . * *

FIGURE 26

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
 GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
 TCTAACTACGTGTTTCGCACTACCAAATTCAGAGAAAATAGCATTACCATGCCTTCCTGG
 TGACTIONAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
 ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
 TCTTTTTTGGCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGAAAAT
 GTTCCACAGTTTGGTCCGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
 TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
 GCCGCCAAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
 ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAAATTCCTCTTC
 TTTTTTCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
 GAGAGAAGCTATTTTTCCCAAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
 TAATTTGACGCTGCAAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
 GAATAGTATTTGCCCACCATTTGGAAGGGACCGTATTGGACTTGTTCGCATTTGAGTAGGCA
 ATCACCAAAGGAACGAGTCTTGAAATTTATCATTTGTTATTTTACAGAAGTTATTACCCCA
 AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
 AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTGAAAAAGTTAAGATTAAA
 GGATTTTCGGTGGTTGTTTCAATTTCTGATATTTGGTTTACCAAGCACAAATTTGAAAACCTT
 GAATCAATTGGCGATTTGTTTCAATTCCTGGCTATTTAGACAACTAATTCCTAAAATTAT
 ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
 TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGCTACTTAGT
 CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
 AATGAGGATTATACCAAAAAAAGTAATAAGTAGTTTCAGGATTATTGCCATCCCATGCAG
 AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
 CACTCAAAAAATTTTGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
 TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
 TAATAATGTCTTACCAGAGCTTTATTTTATGAAATTTGATGTCAAATCTTGCTATGATTC
 CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGT
 TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
 TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
 TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAACAGCTTT
 GTGGGTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC
 TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
 CAGTCCTAGCCAGGACACATTAATTTTAAACTGGCTGACGATTTCTTTATAATATCAAC
 AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
 TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
 TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG
 CACAATGAATAATTTCCATATCCGTTGAAATCTAGTAAAGGGATATTTCGAAGTTTAAAT
 AGCGCTGTTTAACTAGAAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
 CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCCGAATGTTATAAATCTGC
 TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTATTCTGTTCTTACAACG
 CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
 TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA
 ATTTAAAGATAATATCATTCCTTTTGAGAAAGGAAATTCACACTTGCAAGC

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FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHQREARPA LLTSRLRFIPKPDGLRPVNM DYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHQREARPA LLTSRLRFIPKPDGLRPVNM DYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

[illegible]

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA
AGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC
GTGCTCAACTACGAGCGGGCGCG

FIGURE 29

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV
STFPNYLISILESKNWQLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK
RTIETSITQNK SARKEVSWNSISIRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMLQWIFPRQFG
LINAQVVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL
GKR SNAKMCLSDFEKRKQIFAEFIYWL YNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT
SMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLKRFLIKMGSNKKMLVSTNQT
LRPVASILKHLNEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR
IVKKKLDPEFVIRKYATI HATSDRATKNFVSEAFSYFDMVPFEKV VQLLSMKTSDTL FVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVD DFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNCCNI
YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVFLHRRJAD

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FIGURE 30'

ggtaccgatttactttcttctcataagciaattgcttctcgaacgctcctaaatctctggaaatattttacaagaactcaataacaataccaagtcaaattccaatatgaagg
 tgttattagtatcgataatatttctattttatcggtcgttaccagataaggacaaaaagaacaacttctctcccctaagacttttacttttaatttacttttcaaatatatttcg
 ggttcgcttacttttaacgttggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgctattggatagctcttggagtagctcacagaaatccttacaatctt
 ctgatgagactatattagattcattacagtcggtgcatattcttaacatggagccttacacttttagatgagtcacgctcgatgaggtatttggatcalccaacgtttgccttg
 aaaaggttgataaattttgcaaatcatgctcttagtggtggaatccgcgaaagtgtttgatgcttcacacgcttagcatgattgagatattcaaaaatttctaccactaca
 ctctttaacgcggtttatttttctattttctattctcatgttgttccaaatagtatcatctcgtattaggctttttcgttttactcctggaatcgtaaccttttctacttcccctaag
 aataatctaaattagtttcgctataattgatagtagtagaagattggtgattctactcgttaattgttattagtttaaagatactttgcaaaacatttattagctatcattatataaaa
 aaaatcctataaattataaataatcaatatttgcggtcactatttattaaacgttatgatcagtaggacactttgcatatatatagttatgcttaattggttacttgaacttgcAT
 GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTAT
 CCTTAAATGATTATGTACAACCTTGTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAA
 CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTCTTCATTTCGACTGTAGTCGGCTTCGACAGT
 AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGGtatatatattttgtttgattttttctattcg
 ggatagctaataatattgggcagCTAATAGCGAATGTTGTAAAACAGATGTTTCGATGAAAGTTTGGAGCGTCGAAGGA
 ATCTACTGATGAAAGGGTTTTCCATGgtaaggtattctaattgtgaaatatttaccctgcaattactgtttcaaagagattgtatttaaccgataaagAA
 TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCTAATTA
 CCTTATATCTATACTTGAGTCAAAAAATTGGCAACTTTTGTAGAAA Tgtaaataccgggttaagattgttcgcactttgaa
 agactgacaagtagTATCGGCAGTGTGCCATGCATTACTTATTATCCAAAGGAAGTATTTTGGAGGCTCTTC
 CAAATGACAATTACCTTCAGATTTCTGGCATACCACTTTTAAAAATAATGTGTTTGGAGAAAAGTGTGT
 CAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAATAAAAGCGCCCCGAAAGAAGTTTC
 CTGGAATAGCATTTCATTTAGTAGGTTTAGCATTTTTACAGGTCATCCTATAAGAAGTTTAAAGCAAGgt
 aactaactgttactcctcataactaatttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG
 TGGCTTCAATGGATTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA
 AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCCTAAAGGTATACCTTTAATTGA
 ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA
 CACCCACGATGATGAAAAATCCTTAGTTATTCTTAAAGCCGAACCAGGTGTTTGCCTTCTTCGATC
 CATTCTTGTTTCGAGTGTTCCTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAGG
 tattgtataaaatttaccactaacgattttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC
 ATTATTTAATGAGTAACATAAAAGtaaatgccaatttttaccattaattaacaatcagATTTTCAGAAATTGAATGGCTAGT
 CCTTGGAAGAAAGGTCAAAATGCGAAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAAATATTTGCGG
 AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTTATATCACTGAATC
 AAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTTGGAAACTCTTGTCGCCACCCTTTAT
 TACATCAATGAAAATGGAAGCGTTTGAAAAATAAACGAGGtattttaagatttttgcataaatattttcagAACAA
 TGTTAGGATGGATACTCAGAAAACACTTTGCCTCCAGCAGTTATTCGCTATTACCTAAGAAGAATAC
 CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAAGtattttaattttgtcatcaatgtacttacttctaactattattag
 cagATGGGTTCAAAACAAAAAATGTTAGTCAGTACGAACCAAACTTTACGACCTGTGGCATCGATACTG
 AAACATTTAATCAATGAAGAAAGTAGTGGTATTCATTTAACTTGAGGTTTACATGAAGCTTCTTACT
 TTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGgtaattatataatgcgcgattcctcattattaattttcagCGCTAAGAAG
 TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT
 AAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCG
 AGCTACAAAAAATTTGTTAGTGAGGCGTTTCTCTATGAAAACATCAGATACTTTGTTTGTGATTGTTGT
 GGTGCCTTTTGAAGAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTGATTGTTGT
 GGATTATTGGACCAAAAGTTCTTCTGAAATTTTTAAAAATGCTCAAGGAACATCTCTCTGGACACATTGT
 TAAGtataccaattgttgaattgaataacactaatgaactagATAGGAAATTTCTCAATACCTTCAAAAAGTTGGTATCCCTC
 AGGGCTCAATTCTGTCTCTTTTTTGTGTCATTCTATATGGAAGATTGATTGATGAATACCTATACGTT
 TACGAAAAAAGAAAGGATCAGTGTGTTACGAGTAGTCGACGATTTCTCTTTATAACAGTTAATAAAA
 AGGATGCAAAAAATTTTTGAATTTATCTTTAAGAGTgtgagtgctgctcattcctaagtttaaccgttgaagGATTTGAGAA
 ACACAATTTTTCTACGAGCCTGGAGAAAACAGTAATAAACTTTGAAAATAGTAATGGGATAATAAACA
 ATACTTTTTTAATGAAAGCAAGAAAAGAAAGCCATTCTTCGGTTTCTCTGTGAACATGAGGTCTCTTG
 ATACATTGTTAGCATGCTCTAAAATTGATGAAGCCTATTTAACTCTACATCTGTAGAGCTGACGAAAC
 ATATGGGGAATCTTTTTTTTACAAAATTCTAAAGtatactgtgaactgaataatagctgacaaataatcagATCGAGCCTTGC
 ATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCAATTTCTTGCTGCAATATATATAG
 GCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCC
 AAAGAATGTTTCATAACGGgtgagtagtatttttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAAA
 ATTTGGAAGAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCTCTGCAGAAGTCAA

[illegible]

FIGURE 31

| | | |
|---------------------|--|-----|
| EST2 pep | FFYCTEISST VTIVYFRHDT WN---KLIT P-----FIVE YFK-TYLVEN | 40 |
| Euplotes pep | FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS IAD----LKK ETLA--EVQE | 43 |
| Trans of tetrahymen | -----KHKE GSQIFYRKP IWKLVSCLTI VKVRIQFSEK NKQMKQNFYQ | 44 |
| Consensus | FFY.TE..K. .S..YYRK. IW...-KL..-F..KV.. | 50 |
| | | |
| EST2 pep | NVCRNHNSY- ----- TLSNFNHSM FRIIPKKSNE FRIIPKKSNE | 79 |
| Euplotes pep | KEVEEWKSL ----- ---GFAPGKE FRIIPKKT FRIIPKKT | 78 |
| Trans of tetrahymen | KIQLEENLE KVEEKLIPED SPQKYPQCKL FRIIPKKS FRIIPKKS | 92 |
| Consensus | K...E..... -----F..GKC FRIIPKKS FRIIPKKS | 100 |
| | | |
| EST2 pep | ADEEEFTIYK ENHKNAIQPT QKILEYERNK RPTSFTKIYS PTQLADRIKE | 129 |
| Euplotes pep | IVNSDRKTTK LTTNTKLLNS HMLMLKTEKN -----RMFK -DPFGFAVFN | 120 |
| Trans of tetrahymen | DKQKNIK--- LNLNQILMDS QLVFRNKKD -----ML-G -QKIGYSVFD | 130 |
| Consensus |K..K LN.N..L..S QL.L..LKN -----...IG..VF.. | 150 |
| | | |
| EST2 pep | FKQRLLRKN NVL----- FEFYFMKFD VKSCYD | 157 |
| Euplotes pep | YD-DVMKRYE EFVCKWKQVG QKIEFFATMD IEKCYD | 155 |
| Trans of tetrahymen | NK-QISEKFA QFIEKWKNKG RFEIYYVTL- ----- | 158 |
| Consensus | .K-...KKF. .F..KWK..G .E..CYF.T.D ...CYD | 186 |

FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: AET FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIGURE 33

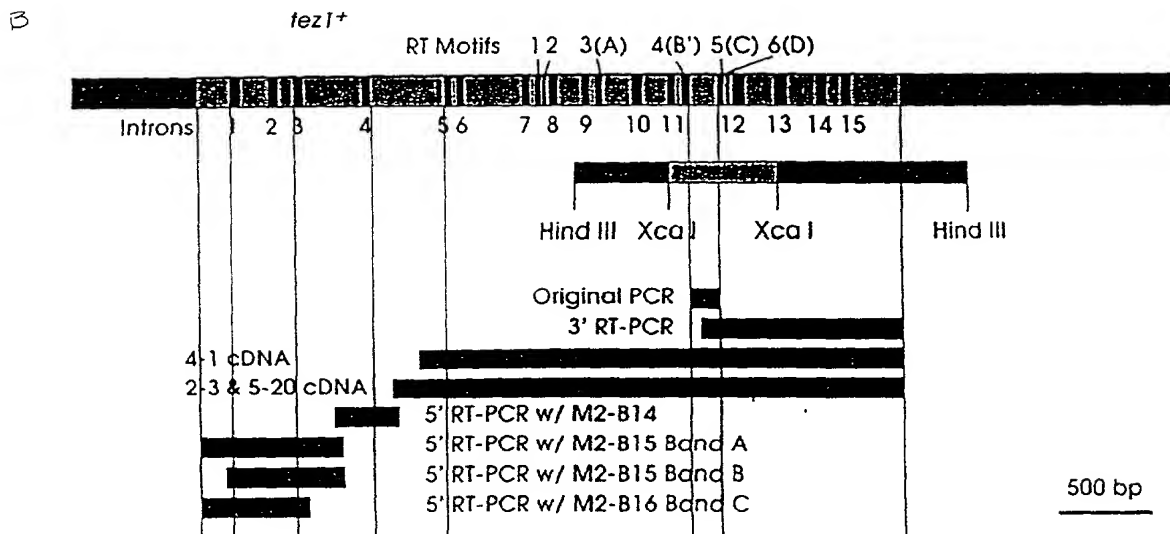
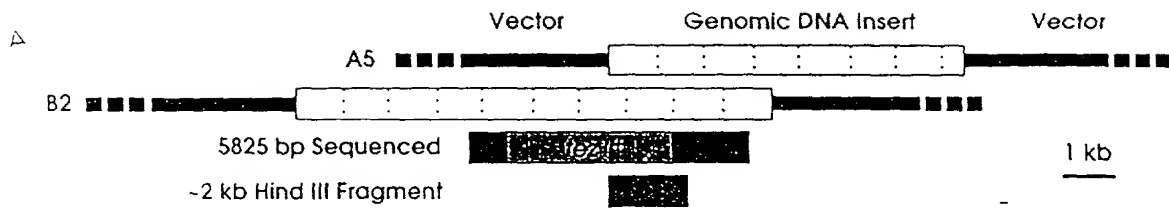


FIGURE 34

Poly 4

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|
| | | | t | | t | | c | | |
| | t | a | a | g | c | c | t | c | g |
| 5'- | cag | acc | aaa | gga | att | cca | taa | gg | -3' |
| | Q | T | K | G | I | P | Q | G | |

4 (B')

5 (c')

| | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | D | D | Y | L | L | I | T | |
| 3'- | ctg | ctg | atg | gag | gag | tag | tgg | -5' |
| | a | a | a | a | a | a | a | |
| | | | t | t | t | t | | |

Poly 1

FIGURE 35

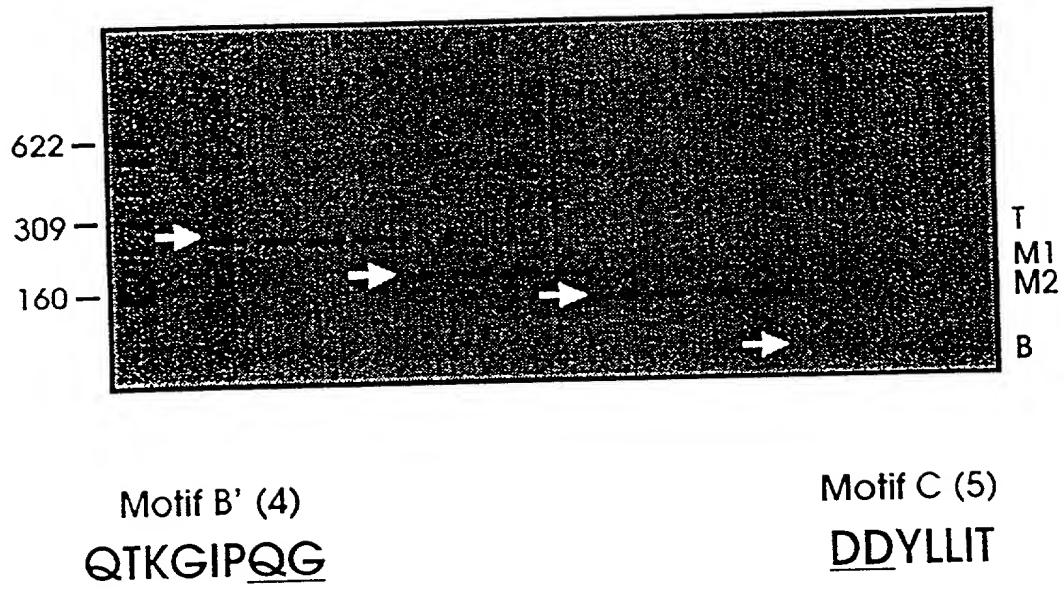


FIGURE 36

PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

| | |
|---------|---|
| Ot | LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT |
| Ea_p123 | KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT |
| Sp_M2 | SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV |
| Sc_p103 | DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS |
| | . * . * . * |

Q K V G I P Q G
 caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

Poly 4

t t c
 a a g c c t c g
 Cag acc aaa gga att cca taa gg ---->
 ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
 tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC
 K G I P S G S I L S S F L C H F Y M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
 CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
 CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

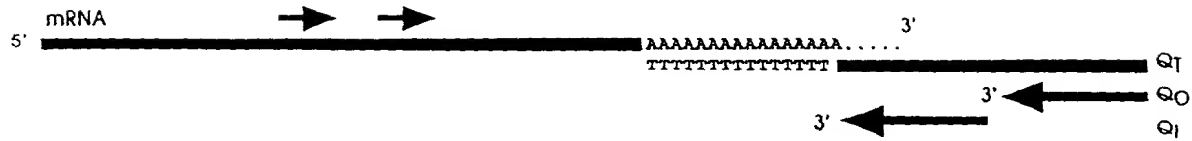
<---- ctg ctg atg gag gag tag tgg
 a a a a a a a a
 t t t t
 c c

Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.
 D D F L F I T

FIGURE 37

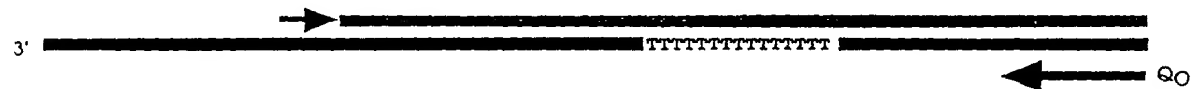
3' RT PCR Strategy



1. Synthesis of cDNA with Q_T Primer.



2. First Round PCR Using Outside Primer and Q_O Primer.



3. Second Round PCR Using Inside Primer and Q_I Primer.



4. Sequence Second Round PCR Products Using Inside Primer or Q_I Primer.

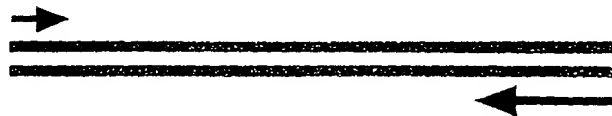


FIGURE 38

A

-Size Selected Libraries from P. Nurese

- 3 ~ 4 kb
- 5 ~ 6 kb
- 7 ~ 8 kb
- 11 ~ 12 kb

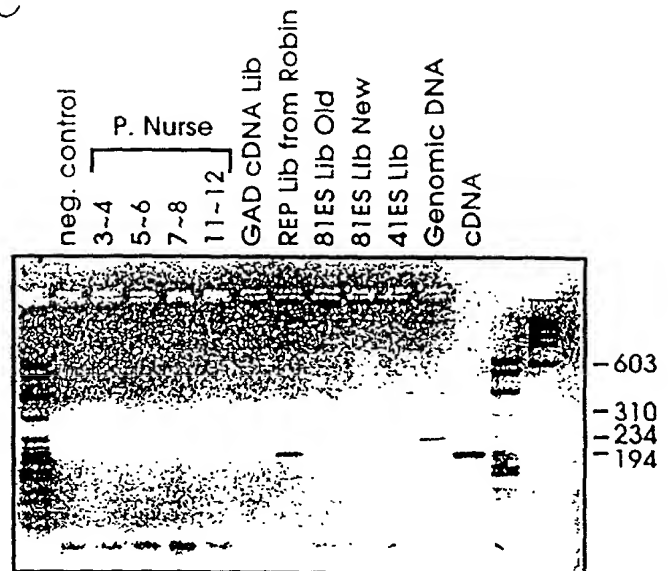
-Libraries from J.A. Wise

- Sau 3a Partial Digest
- Hind III Partial Digest

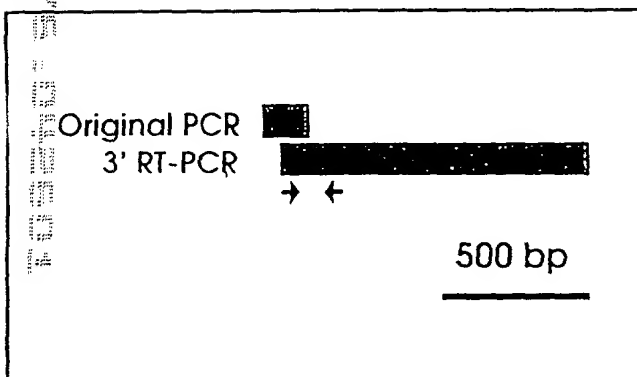
cDNA Libraries

- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

C



B



D

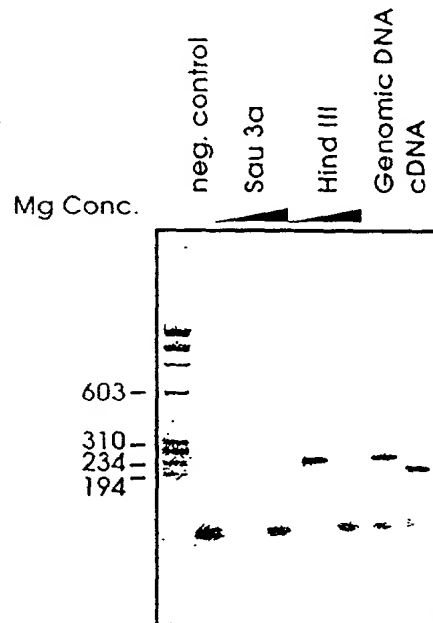


FIGURE 39

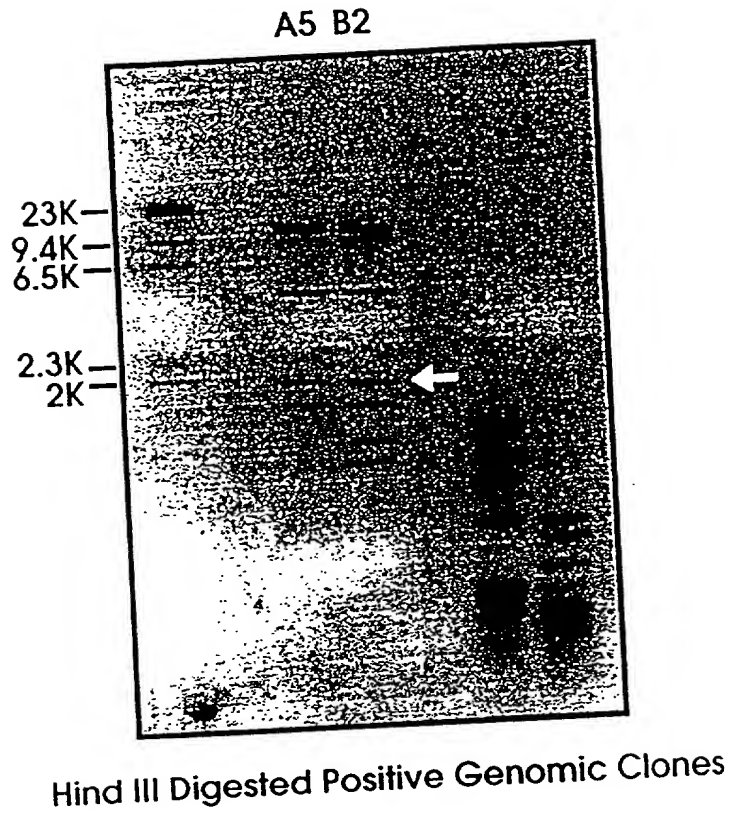
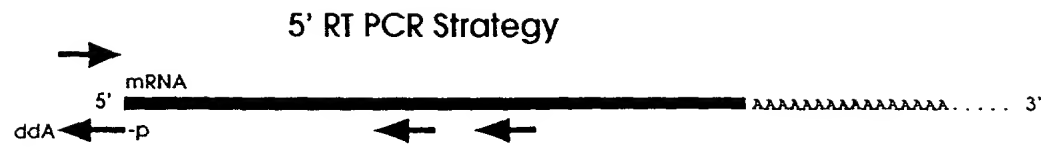
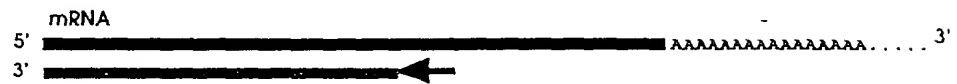


FIGURE 40



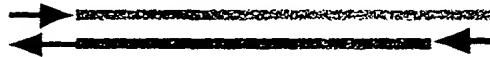
1. Synthesis of cDNA with Specific Downstream Primer.



2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR

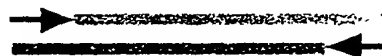


FIGURE 41

Alignment of RT Domains from Telomerase Catalytic Subunits.

```

                                Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ... (35) ...
S.c. Est2p (366). WLFRLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ... (35) ...
E.a. p123 (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ... (35) ...
      *          *** **          * * *

      Motif 1      Motif 2      K
      p hh h K      hR h      R
S.p. Tez1p AVIRLLPKK--NTFRLITN-LRKRF ... (61) ...
S.c. Est2p SKMRIIPKKSNNEFRIIAIPCRGAD ... (62) ...
E.a. p123 GKLRLIPKK--TTFRPIMTFNKKIV ... (61) ...
      *   ***   ** *

      Motif 3(A) AF
      h hDh GY h
S.p. Tez1p KKYFVRIDIKSCYDRIKQDLMFRIVK ... (89) ...
S.c. Est2p ELYFMKFDVKSCYDSIPRMECMRILK ... (75) ...
E.a. p123 KLFATMDIEKCYDSVNREKLSTFLK ... (107) ...
      *   *   ***   *

      Motif 4(B')
      hPQG pP hh h
S.p. Tez1p YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ... (6) ...
S.c. Est2p YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ... (8) ...
E.a. p123 YKQTKGIPQGLCVSSILSSFYATLEESSLGF ... (14) ...
      *   *   **   *   *   *

      Y Motif 5(C)      Motif 6(D)
      h F DDhnh      Gh h cK h
S.p. Tez1p VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEEKHNFSTSLKTVINFENS . (205)
S.c. Est2p LILKLADDFLIISTDQQQVINIKKLLAMGGFQKYNAKANRDKILAVSSQS . (173)
E.a. p123 LLMPLETDYLLITTQENNAVLFIKLINVSRENGFKFNMKKLQTSFPLS . (209)
      ** * *          *   *

```

FIGURE 42

A

Sp_Tp1p 1MTEHNTPKSRILRFLNENGYVYLC 2
 Sc_Eat2p 1MKILFEF 7
 Ea_p123 1 MEVDYDNOADNHGINSALKTCCEIKKAE 7 YSW 20

Sp_Tp1p 74 LNYVYLYRQSPALSNICRERSDVOTSS 47
 Sc_Eat2p 74MKKCGH HGLD 24
 Ea_p123 74 MKVIRCRN 30DLEDIKI AQTN 41

Sp_Tp1p 74 FVHSTYVYDFD KPDFOVQVSSPKC 40 AN 40
 Sc_Eat2p 74 FVHSTYVYDFD KPDFOVQVSSPKC 40 AN 40
 Ea_p123 74 FVHSTYVYDFD KPDFOVQVSSPKC 40 AN 40

Sp_Tp1p 11 VYKQFDE FERRN LKMK SMNHDFRANH 127
 Sc_Eat2p 11 VYKQFDE FERRN LKMK SMNHDFRANH 127
 Ea_p123 11 VYKQFDE FERRN LKMK SMNHDFRANH 127

Sp_Tp1p 112 VNGQVNDLVSTFPHNYLISILESKN 166
 Sc_Eat2p 112 VNGQVNDLVSTFPHNYLISILESKN 166
 Ea_p123 112 VNGQVNDLVSTFPHNYLISILESKN 166

Sp_Tp1p 158 SDHMY LSKGSI FALPHDNYL 158 IPLFKH 166
 Sc_Eat2p 158 SDHMY LSKGSI FALPHDNYL 158 IPLFKH 166
 Ea_p123 158 SDHMY LSKGSI FALPHDNYL 158 IPLFKH 166

Sp_Tp1p 158 HYFEETYSK KRTIETSI TONKSARKE 214
 Sc_Eat2p 158 HYFEETYSK KRTIETSI TONKSARKE 214
 Ea_p123 158 HYFEETYSK KRTIETSI TONKSARKE 214

Sp_Tp1p 210 WNSISIRFSIFRSSY KGOYELHICD 261
 Sc_Eat2p 210 WNSISIRFSIFRSSY KGOYELHICD 261
 Ea_p123 210 WNSISIRFSIFRSSY KGOYELHICD 261

Sp_Tp1p 210 RNTVHMWLOWIFPROGLINAFQYKLNKVIPL 261
 Sc_Eat2p 210 RNTVHMWLOWIFPROGLINAFQYKLNKVIPL 261
 Ea_p123 210 RNTVHMWLOWIFPROGLINAFQYKLNKVIPL 261

Sp_Tp1p 260 VSOSTVYVPRLL YPLEQTA LHM 313
 Sc_Eat2p 260 VSOSTVYVPRLL YPLEQTA LHM 313
 Ea_p123 260 VSOSTVYVPRLL YPLEQTA LHM 313

Sp_Tp1p 314 LSKYVHY YID ND EKI YSLKPN 342
 Sc_Eat2p 314 LSKYVHY YID ND EKI YSLKPN 342
 Ea_p123 314 LSKYVHY YID ND EKI YSLKPN 342

Sp_Tp1p 342FALLRSILYVYF KLI 360
 Sc_Eat2p 342FALLRSILYVYF KLI 360
 Ea_p123 342FALLRSILYVYF KLI 360

Sp_Tp1p 360 WGNORIFEIIL DLETLF LSKYVHY 360
 Sc_Eat2p 360 WGNORIFEIIL DLETLF LSKYVHY 360
 Ea_p123 360 WGNORIFEIIL DLETLF LSKYVHY 360

Sp_Tp1p 400 NIKISEIIL YLQKRSNAKMLC 400 KKKOIFA 400
 Sc_Eat2p 400 NIKISEIIL YLQKRSNAKMLC 400 KKKOIFA 400
 Ea_p123 400 NIKISEIIL YLQKRSNAKMLC 400 KKKOIFA 400

Sp_Tp1p 400 EFIVLYNSFIIPLOSSSDLNHY 400
 Sc_Eat2p 400 EFIVLYNSFIIPLOSSSDLNHY 400
 Ea_p123 400 EFIVLYNSFIIPLOSSSDLNHY 400

Sp_Tp1p 400 FDKI LKLCRPF TSMKMEAFKIMENHYMD 400
 Sc_Eat2p 400 FDKI LKLCRPF TSMKMEAFKIMENHYMD 400
 Ea_p123 400 FDKI LKLCRPF TSMKMEAFKIMENHYMD 400

Sp_Tp1p 400 TOKTTLPPAVILHT LTNLRKFL 400
 Sc_Eat2p 400 TOKTTLPPAVILHT LTNLRKFL 400
 Ea_p123 400 TOKTTLPPAVILHT LTNLRKFL 400

Sp_Tp1p 400 IKMOSKMKIYSTHOLRPFYASIKHIE 400
 Sc_Eat2p 400 IKMOSKMKIYSTHOLRPFYASIKHIE 400
 Ea_p123 400 IKMOSKMKIYSTHOLRPFYASIKHIE 400

Sp_Tp1p 400 ESSGIPFNLEYVYKLLTFFKDLHMFGR 400
 Sc_Eat2p 400 ESSGIPFNLEYVYKLLTFFKDLHMFGR 400
 Ea_p123 400 ESSGIPFNLEYVYKLLTFFKDLHMFGR 400

Sp_Tp1p 400 VYRI IKS RIKKOLMFRI KKKOPE 400
 Sc_Eat2p 400 VYRI IKS RIKKOLMFRI KKKOPE 400
 Ea_p123 400 VYRI IKS RIKKOLMFRI KKKOPE 400

Sp_Tp1p 400 VIKRYATINATSDRATK 400
 Sc_Eat2p 400 VIKRYATINATSDRATK 400
 Ea_p123 400 VIKRYATINATSDRATK 400

Sp_Tp1p 400 FYSEAFSYDFMYPFK VOLSMKTSDT 400
 Sc_Eat2p 400 FYSEAFSYDFMYPFK VOLSMKTSDT 400
 Ea_p123 400 FYSEAFSYDFMYPFK VOLSMKTSDT 400

Sp_Tp1p 400 DFVDYVTKSSSEIFKMLKNSOHIVKIGNSO 400
 Sc_Eat2p 400 DFVDYVTKSSSEIFKMLKNSOHIVKIGNSO 400
 Ea_p123 400 DFVDYVTKSSSEIFKMLKNSOHIVKIGNSO 400

Sp_Tp1p 400 LOKV IPI SIL SFLCHFYMD IDEYLS 400
 Sc_Eat2p 400 LOKV IPI SIL SFLCHFYMD IDEYLS 400
 Ea_p123 400 LOKV IPI SIL SFLCHFYMD IDEYLS 400

Sp_Tp1p 400 KKGSVLLRYV F TYNKKDAKK 400
 Sc_Eat2p 400 KKGSVLLRYV F TYNKKDAKK 400
 Ea_p123 400 KKGSVLLRYV F TYNKKDAKK 400

Sp_Tp1p 400 FNLSLRGFEKHNFTSL TVINFEN 400
 Sc_Eat2p 400 FNLSLRGFEKHNFTSL TVINFEN 400
 Ea_p123 400 FNLSLRGFEKHNFTSL TVINFEN 400

Sp_Tp1p 400 IINHTFESKKNPF FVHRSOTLL 400
 Sc_Eat2p 400 IINHTFESKKNPF FVHRSOTLL 400
 Ea_p123 400 IINHTFESKKNPF FVHRSOTLL 400

Sp_Tp1p 400 ACPRIDEALFNSTSYELTKHMKSSFF 400
 Sc_Eat2p 400 ACPRIDEALFNSTSYELTKHMKSSFF 400
 Ea_p123 400 ACPRIDEALFNSTSYELTKHMKSSFF 400

Sp_Tp1p 400 ASFAQVFIIDTHSKFNSSCCHIVLGYSCMHR 400
 Sc_Eat2p 400 ASFAQVFIIDTHSKFNSSCCHIVLGYSCMHR 400
 Ea_p123 400 ASFAQVFIIDTHSKFNSSCCHIVLGYSCMHR 400

Sp_Tp1p 400 ADAYLRRK IFIPORMFIDLLNVIOR 400
 Sc_Eat2p 400 ADAYLRRK IFIPORMFIDLLNVIOR 400
 Ea_p123 400 ADAYLRRK IFIPORMFIDLLNVIOR 400

Sp_Tp1p 400 LAEILQYTSRRFLSSAEVWFLCGLMRD 400
 Sc_Eat2p 400 LAEILQYTSRRFLSSAEVWFLCGLMRD 400
 Ea_p123 400 LAEILQYTSRRFLSSAEVWFLCGLMRD 400

Sp_Tp1p 400 FKYNPCFEOLIO QSLTDILPLRPV 400
 Sc_Eat2p 400 FKYNPCFEOLIO QSLTDILPLRPV 400
 Ea_p123 400 FKYNPCFEOLIO QSLTDILPLRPV 400

Sp_Tp1p 400 LNRRIAD 400
 Sc_Eat2p 400 LNRRIAD 400
 Ea_p123 400 LNRRIAD 400

B

Sp_Tp1p 1MTEHNTPKSRILRFLNENGYVYLC 2
 Sc_Eat2p 1MKILFEF 7
 Ea_p123 1 MEVDYDNOADNHGINSALKTCCEIKKAE 7 YSW 20

Sp_Tp1p 74 LNDYVYLYRQSPALSNICERLRSVDYOTSS 11
 Sc_Eat2p 74 LNDYVYLYRQSPALSNICERLRSVDYOTSS 11
 Ea_p123 74 LNDYVYLYRQSPALSNICERLRSVDYOTSS 11

Sp_Tp1p 74 IFHSTYVYDFD KPDFOVQVSSPKC 40 AN 40
 Sc_Eat2p 74 IFHSTYVYDFD KPDFOVQVSSPKC 40 AN 40
 Ea_p123 74 IFHSTYVYDFD KPDFOVQVSSPKC 40 AN 40

Sp_Tp1p 74 VYKQFDE FERRN LKMK SMNHDFRANH 127
 Sc_Eat2p 74 VYKQFDE FERRN LKMK SMNHDFRANH 127
 Ea_p123 74 VYKQFDE FERRN LKMK SMNHDFRANH 127

Sp_Tp1p 112 VNGQVNDLVSTFPHNYLISILESKN 166
 Sc_Eat2p 112 VNGQVNDLVSTFPHNYLISILESKN 166
 Ea_p123 112 VNGQVNDLVSTFPHNYLISILESKN 166

Sp_Tp1p 158 SDHMY LSKGSI FALPHDNYL 158 IPLFKH 166
 Sc_Eat2p 158 SDHMY LSKGSI FALPHDNYL 158 IPLFKH 166
 Ea_p123 158 SDHMY LSKGSI FALPHDNYL 158 IPLFKH 166

Sp_Tp1p 158 HYFEETYSK KRTIETSI TONKSARKE 214
 Sc_Eat2p 158 HYFEETYSK KRTIETSI TONKSARKE 214
 Ea_p123 158 HYFEETYSK KRTIETSI TONKSARKE 214

Sp_Tp1p 210 WNSISIRFSIFRSSY KGOYELHICD 261
 Sc_Eat2p 210 WNSISIRFSIFRSSY KGOYELHICD 261
 Ea_p123 210 WNSISIRFSIFRSSY KGOYELHICD 261

Sp_Tp1p 210 RNTVHMWLOWIFPROGLINAFQYKLNKVIPL 261
 Sc_Eat2p 210 RNTVHMWLOWIFPROGLINAFQYKLNKVIPL 261
 Ea_p123 210 RNTVHMWLOWIFPROGLINAFQYKLNKVIPL 261

Sp_Tp1p 260 VSOSTVYVPRLL YPLEQTA LHM 313
 Sc_Eat2p 260 VSOSTVYVPRLL YPLEQTA LHM 313
 Ea_p123 260 VSOSTVYVPRLL YPLEQTA LHM 313

Sp_Tp1p 314 LSKYVHY YID ND EKI YSLKPN 342
 Sc_Eat2p 314 LSKYVHY YID ND EKI YSLKPN 342
 Ea_p123 314 LSKYVHY YID ND EKI YSLKPN 342

Sp_Tp1p 342FALLRSILYVYF KLI 360
 Sc_Eat2p 342FALLRSILYVYF KLI 360
 Ea_p123 342FALLRSILYVYF KLI 360

Sp_Tp1p 360 WGNORIFEIIL DLETLF LSKYVHY 360
 Sc_Eat2p 360 WGNORIFEIIL DLETLF LSKYVHY 360
 Ea_p123 360 WGNORIFEIIL DLETLF LSKYVHY 360

Sp_Tp1p 400 NIKISEIIL YLQKRSNAKMLC 400 KKKOIFA 400
 Sc_Eat2p 400 NIKISEIIL YLQKRSNAKMLC 400 KKKOIFA 400
 Ea_p123 400 NIKISEIIL YLQKRSNAKMLC 400 KKKOIFA 400

Sp_Tp1p 400 EFIVLYNSFIIPLOSSSDLNHY 400
 Sc_Eat2p 400 EFIVLYNSFIIPLOSSSDLNHY 400
 Ea_p123 400 EFIVLYNSFIIPLOSSSDLNHY 400

Sp_Tp1p 400 FDKI LKLCRPF TSMKMEAFKIMENHYMD 400
 Sc_Eat2p 400 FDKI LKLCRPF TSMKMEAFKIMENHYMD 400
 Ea_p123 400 FDKI LKLCRPF TSMKMEAFKIMENHYMD 400

Sp_Tp1p 400 TOKTTLPPAVILHT LTNLRKFL 400
 Sc_Eat2p 400 TOKTTLPPAVILHT LTNLRKFL 400
 Ea_p123 400 TOKTTLPPAVILHT LTNLRKFL 400

Sp_Tp1p 400 IKMOSKMKIYSTHOLRPFYASIKHIE 400
 Sc_Eat2p 400 IKMOSKMKIYSTHOLRPFYASIKHIE 400
 Ea_p123 400 IKMOSKMKIYSTHOLRPFYASIKHIE 400

Sp_Tp1p 400 ESSGIPFNLEYVYKLLTFFKDLHMFGR 400
 Sc_Eat2p 400 ESSGIPFNLEYVYKLLTFFKDLHMFGR 400
 Ea_p123 400 ESSGIPFNLEYVYKLLTFFKDLHMFGR 400

Sp_Tp1p 400 VYRI IKS RIKKOLMFRI KKKOPE 400
 Sc_Eat2p 400 VYRI IKS RIKKOLMFRI KKKOPE 400
 Ea_p123 400 VYRI IKS RIKKOLMFRI KKKOPE 400

Sp_Tp1p 400 VIKRYATINATSDRATK 400
 Sc_Eat2p 400 VIKRYATINATSDRATK 400
 Ea_p123 400 VIKRYATINATSDRATK 400

Sp_Tp1p 400 FYSEAFSYDFMYPFK VOLSMKTSDT 400
 Sc_Eat2p 400 FYSEAFSYDFMYPFK VOLSMKTSDT 400
 Ea_p123 400 FYSEAFSYDFMYPFK VOLSMKTSDT 400

Sp_Tp1p 400 DFVDYVTKSSSEIFKMLKNSOHIVKIGNSO 400
 Sc_Eat2p 400 DFVDYVTKSSSEIFKMLKNSOHIVKIGNSO 400
 Ea_p123 400 DFVDYVTKSSSEIFKMLKNSOHIVKIGNSO 400

Sp_Tp1p 400 LOKV IPI SIL SFLCHFYMD IDEYLS 400
 Sc_Eat2p 400 LOKV IPI SIL SFLCHFYMD IDEYLS 400
 Ea_p123 400 LOKV IPI SIL SFLCHFYMD IDEYLS 400

Sp_Tp1p 400 KKGSVLLRYV F TYNKKDAKK 400
 Sc_Eat2p 400 KKGSVLLRYV F TYNKKDAKK 400
 Ea_p123 400 KKGSVLLRYV F TYNKKDAKK 400

Sp_Tp1p 400 FNLSLRGFEKHNFTSL TVINFEN 400
 Sc_Eat2p 400 FNLSLRGFEKHNFTSL TVINFEN 400
 Ea_p123 400 FNLSLRGFEKHNFTSL TVINFEN 400

Sp_Tp1p 400 IINHTFESKKNPF FVHRSOTLL 400
 Sc_Eat2p 400 IINHTFESKKNPF FVHRSOTLL 400
 Ea_p123 400 IINHTFESKKNPF FVHRSOTLL 400

Sp_Tp1p 400 ACPRIDEALFNSTSYELTKHMKSSFF 400
 Sc_Eat2p 400 ACPRIDEALFNSTSYELTKHMKSSFF 400
 Ea_p123 400 ACPRIDEALFNSTSYELTKHMKSSFF 400

Sp_Tp1p 400 ASFAQVFIIDTHSKFNSSCCHIVLGYSCMHR 400
 Sc_Eat2p 400 ASFAQVFIIDTHSKFNSSCCHIVLGYSCMHR 400
 Ea_p123 400 ASFAQVFIIDTHSKFNSSCCHIVLGYSCMHR 400

Sp_Tp1p 400 ADAYLRRK IFIPORMFIDLLNVIOR 400
 Sc_Eat2p 400 ADAYLRRK IFIPORMFIDLLNVIOR 400
 Ea_p123 400 ADAYLRRK IFIPORMFIDLLNVIOR 400

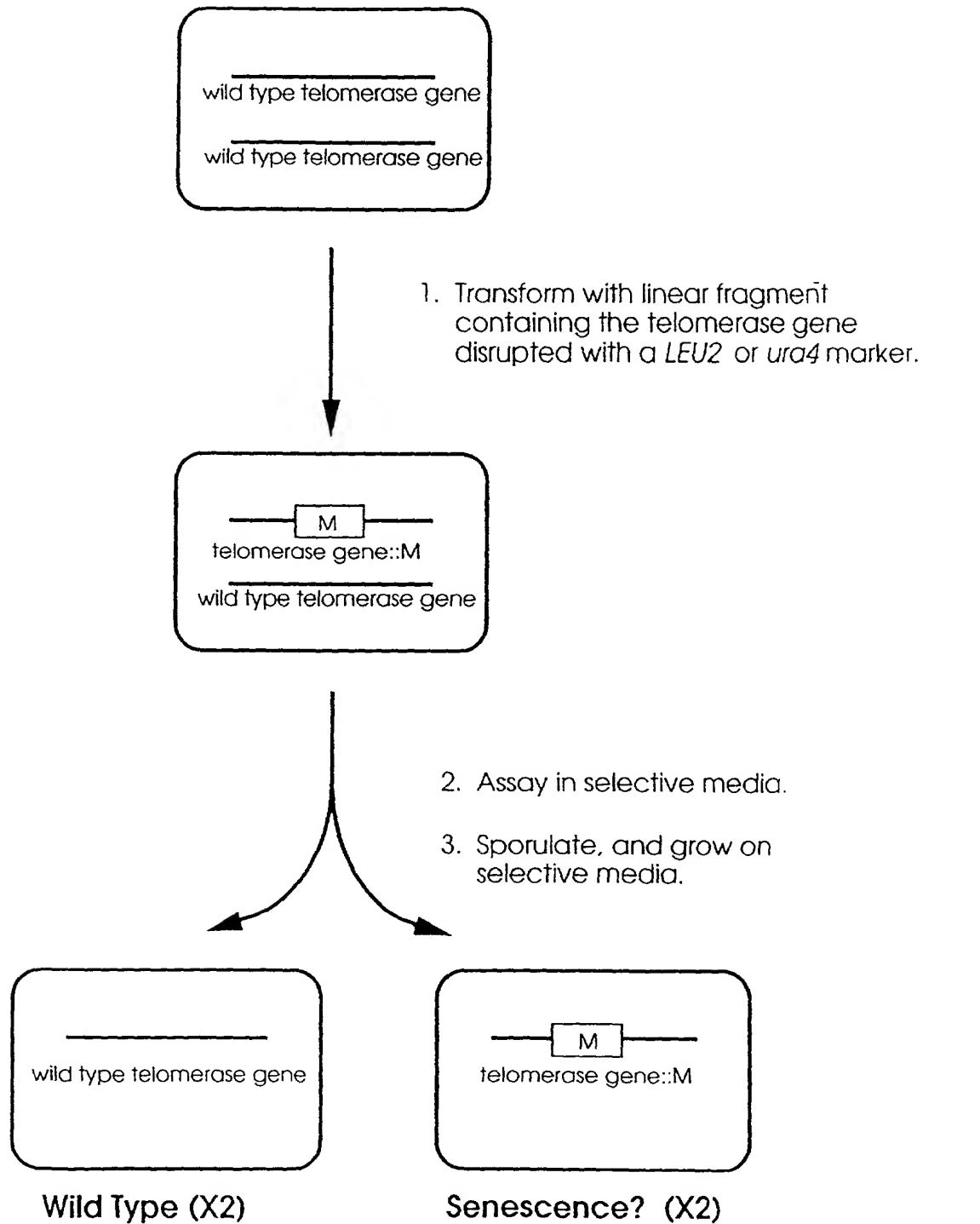
Sp_Tp1p 400 LAEILQYTSRRFLSSAEVWFLCGLMRD 400
 Sc_Eat2p 400 LAEILQYTSRRFLSSAEVWFLCGLMRD 400
 Ea_p123 400 LAEILQYTSRRFLSSAEVWFLCGLMRD 400

Sp_Tp1p 400 FKYNPCFEOLIO QSLTDILPLRPV 400
 Sc_Eat2p 400 FKYNPCFEOLIO QSLTDILPLRPV 400
 Ea_p123 400 FKYNPCFEOLIO QSLTDILPLRPV 400

Sp_Tp1p 400 LNRRIAD 400
 Sc_Eat2p 400 LNRRIAD 400
 Ea_p123 400 LNRRIAD 400

FIGURE 43

Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIGURE 44

An Example of Confirmation of *tez1* disruption By PCR

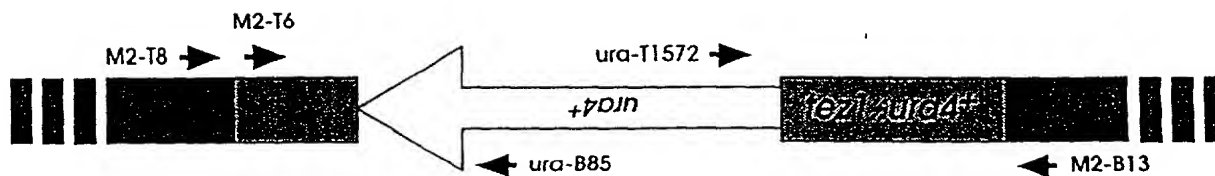
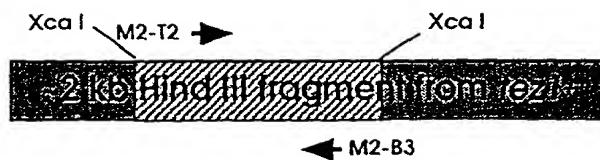
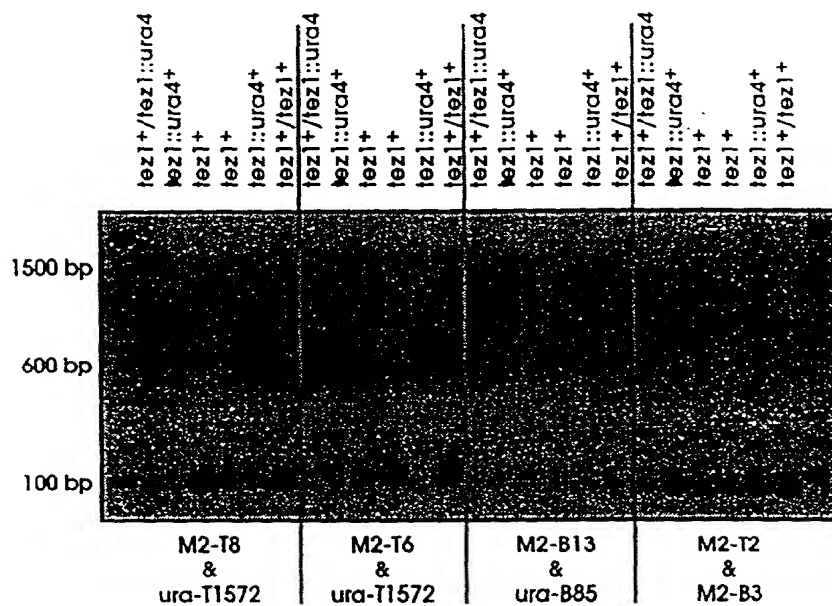


FIGURE 45

Tez1 disruption causes progressive shortening of telomeres in *S. pombe*

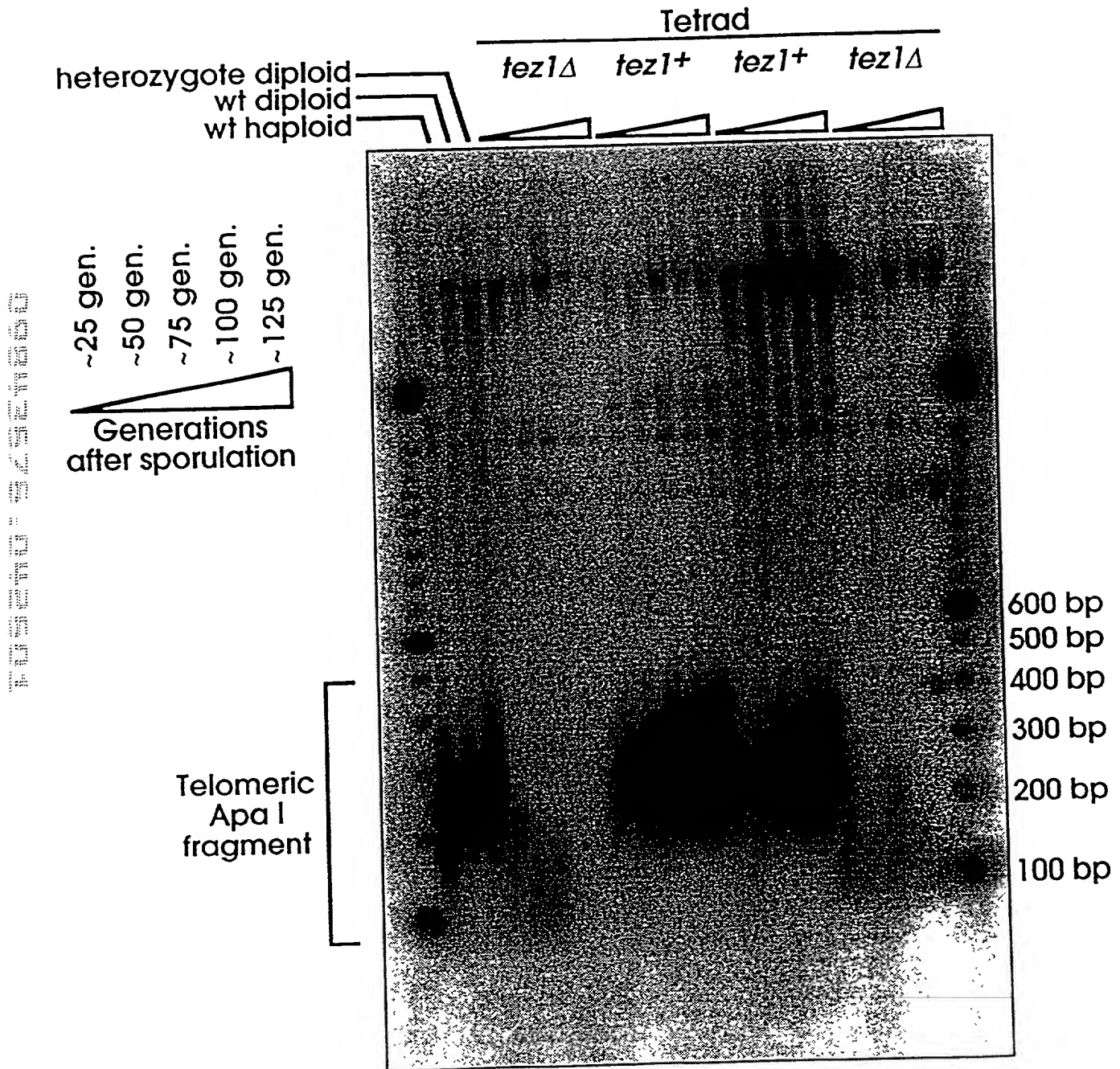


FIGURE 46

1 ggtagcgatttacttttctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatattttttacaaga 80
81 actcaataacaataccaagtcaaattccaatatgaagggtgttatttagtgatcgataatattttctattttatcggtcgta 160
161 ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttactttattaatttacttttcaaataatatttcg 240
241 ggttcgcttactttttaatcgtggtactgttttagctgctacttctagccaaccgctgttttctaccccgctcattggatat 320
321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtcctgcatattc 400
401 ttaacatggagccttacacttttagatgagtcacgtcgcatgatggagtattttggtatcatccaacgtttgcccttgaaaag 480
481 gttgataattattttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttggatgcttgcacacgtctagcatg 560
561 attgagatattcaaaaatttctatccactacaactcctttaacgcgggttttatttttctattttctattctcatgttggt 640
641 ccaaatatgtatcatctcgtatttaggcttttttccggttttactcctggaatcgtaacctttttcactattccccctaata 720
721 ataactctaaattagtttcgcttataattgatagtagtagaaagattgggtgattctactcgtgtaatgttattagttttaa 800
801 gatacttttgcaaaacatttatttagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
881 actattttattttaaaacggttatgatcagtaggacactttgcatatatatagtttatgcttaatggttacttgtaacttgc 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
1 M T E H H T P K S R I L R F L E N Q Y V 20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
21 Y L C T L N D Y V Q L V L R G S P A S S 40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
41 Y S N I C E R L R S D V Q T S F S I F L 60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
61 H S T V V G F D S K P D E G V Q F S S P 80

FIGURE 46 (cont.)

| | | | |
|------|---|---|------|
| 1199 | AAA TGC TCA CAG TCA GAG | gtatatatatattttgttttgatttttttctatttcgggatagctaatatatgggcag | 1272 |
| 81 | K C S Q S E | | 86 |
| 1273 | CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA | 1332 | |
| 87 | L I A N V V K Q M F D E S F E R R R N L | 106 | |
| 1333 | CTG ATG AAA GGG TTT TCC ATG | gtaagggtatttctaattgtgaaatattttacctgcaattactgtttcaaagaga | 1405 |
| 107 | L M K G F S M | 113 | |
| 1406 | ttgtattttaaccgataaag | AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT | 1469 |
| 114 | | N H E D F R A M H V N G V Q N | 128 |
| 1470 | GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA | 1529 | |
| 129 | D L V S T F P N Y L I S I L E S K N W Q | 148 | |
| 1530 | CTT TTG TTA GAA AT | gtaaataccgggttaagatgttgcgactttgaacaagactgacaagtatag T ATC GGC | 1601 |
| 149 | L L L E I | I G | 155 |
| 1602 | AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC | 1661 | |
| 156 | S D A M H Y L L S K G S I F E A L P N D | 175 | |
| 1662 | AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG | 1721 | |
| 176 | N Y L Q I S G I P L F K N N V F E E T V | 195 | |
| 1722 | TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA | 1781 | |
| 196 | S K K R K R T I E T S I T Q N K S A R K | 215 | |
| 1782 | GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT | 1841 | |
| 216 | E V S W N S I S I S R F S I F Y R S S Y | 235 | |
| 1842 | AAG AAG TTT AAG CAA G | gtaactaataactgtttatccttcataactaatttttag AT CTA TAT TTT AAC | |
| 1907 | | | |
| 236 | K K F K Q D | L Y F N | 245 |
| 1908 | TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG | 1967 | |
| 246 | L H S I C D R N T V H M W L Q W I F P R | 265 | |
| 1968 | CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA | 2027 | |
| 266 | Q F G L I N A F Q V K Q L H K V I P L V | 285 | |
| 2028 | TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA | 2087 | |
| 286 | S Q S T V V P K R L L K V Y P L I E Q T | 305 | |
| 2088 | GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT | 2147 | |
| 306 | A K R L H R I S L S K V Y N H Y C P Y I | 325 | |
| 2148 | GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG | 2207 | |
| 326 | D T H D D E K I L S Y S L K P N Q V F A | 345 | |
| 2208 | TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA | 2267 | |
| 346 | F L R S I L V R V F P K L I W G N Q R I | 365 | |
| 2268 | TTT GAG ATA ATA TTA AAA G | gtattgtataaaattttattaccactaacgattttaccag AC CTC GAA ACT | 2336 |
| 366 | F E I I L K D | L E T | 375 |

FIGURE 46 (cont.)

| | | | | | | | | | | | | | | | | | | | | | | |
|------|---|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|------------------------------------|------------------------------|-----|-----|-----|------|-----|-------|------|------|
| 2337 | TTC | TTG | AAA | TTA | TCG | AGA | TAC | GAG | TCT | TTT | AGT | TTA | CAT | TAT | TTA | ATG | AGT | AAC | ATA | AAG | 2396 | |
| 376 | F | L | K | L | S | R | Y | E | S | F | S | L | H | Y | L | M | S | N | I | K | 395 | |
| 2397 | gtaatatgccaaatTTTTTTaccattaattaacaatcag | | | | | | | | | | ATT | TCA | GAA | ATT | GAA | TGG | CTA | GTC | CTT | GGA | 2465 | |
| 396 | | | | | | | | | | | I | S | E | I | E | W | L | V | L | G | 405 | |
| 2466 | AAA | AGG | TCA | AAT | GCG | AAA | ATG | TGC | TTA | AGT | GAT | TTT | GAG | AAA | CGC | AAG | CAA | ATA | TTT | GCG | 2525 | |
| 406 | K | R | S | N | A | K | M | C | L | S | D | F | E | K | R | K | Q | I | F | A | 425 | |
| 2526 | GAA | TTC | ATC | TAC | TGG | CTA | TAC | AAT | TCG | TTT | ATA | ATA | CCT | ATT | TTA | CAA | TCT | TTT | TTT | TAT | 2585 | |
| 426 | E | F | I | Y | W | L | Y | N | S | F | I | I | P | I | L | Q | S | F | F | Y | 445 | |
| 2586 | ATC | ACT | GAA | TCA | AGT | GAT | TTA | CGA | AAT | CGA | ACT | GTT | TAT | TTT | AGA | AAA | GAT | ATT | TGG | AAA | 2645 | |
| 446 | I | T | E | S | S | D | L | R | N | R | T | V | Y | F | R | K | D | I | W | K | 465 | |
| 2646 | CTC | TTG | TGC | CGA | CCC | TTT | ATT | ACA | TCA | ATG | AAA | ATG | GAA | GCG | TTT | GAA | AAA | -ATA | AAC | GAG | 2705 | |
| 466 | L | L | C | R | P | F | I | T | S | M | K | M | E | A | F | E | K | I | N | E | 485 | |
| 2706 | gtattttaaagtattTTTTgcaaaaagctaatttttcag | | | | | | | | | | AAC | AAT | GTT | AGG | ATG | GAT | ACT | CAG | AAA | ACT | 2775 | |
| 486 | | | | | | | | | | | N | N | V | R | M | D | T | Q | K | T | 495 | |
| 2776 | ACT | TTG | CCT | CCA | GCA | GTT | ATT | CGT | CTA | TTA | CCT | AAG | AAG | AAT | ACC | TTT | CGT | CTC | ATT | ACG | 2835 | |
| 496 | T | L | P | P | A | V | I | R | L | L | P | K | K | N | T | F | R | L | I | T | 515 | |
| 2836 | AAT | TTA | AGA | AAA | AGA | TTC | TTA | ATA | AAG | gtattaattTTTTgggtcatcaatgtactttactttctaattctatta | | | | | | | | | | 2906 | | |
| 516 | N | L | R | K | R | F | L | I | K | | | | | | | | | | | 524 | | |
| 2907 | ttagcag | | ATG | GGT | TCA | AAC | AAA | AAA | ATG | TTA | GTC | AGT | ACG | AAC | CAA | ACT | TTA | CGA | CCT | GTG | 2967 | |
| 525 | | | M | G | S | N | K | K | M | L | V | S | T | N | Q | T | L | R | P | V | 542 | |
| 2968 | GCA | TCG | ATA | CTG | AAA | CAT | TTA | ATC | AAT | GAA | GAA | AGT | AGT | GGT | ATT | CCA | TTT | AAC | TTG | GAG | 3027 | |
| 543 | A | S | I | L | K | H | L | I | N | E | E | S | S | G | I | P | F | N | L | E | 562 | |
| 3028 | GTT | TAC | ATG | AAG | CTT | CTT | ACT | TTT | AAG | AAG | GAT | CTT | CTT | AAG | CAC | CGA | ATG | TTT | GG | gtaat | 3088 | |
| 563 | V | Y | M | K | L | L | T | F | K | K | D | L | L | K | H | R | M | F | G | | 581 | |
| 3089 | tatataatgcgcgattcctcattattaattttgcag | | | | | | | | | | G | CGT | AAG | AAG | TAT | TTT | GTA | CGG | ATA | GAT | ATA | 3155 |
| 582 | | | | | | | | | | | | R | K | K | Y | F | V | R | I | D | I | 591 |
| 3156 | AAA | TCC | TGT | TAT | GAT | CGA | ATA | AAG | CAA | GAT | TTG | ATG | TTT | CGG | ATT | GTT | AAA | AAG | AAA | CTC | 3215 | |
| 592 | K | S | C | Y | D | R | I | K | Q | D | L | M | F | R | I | V | K | K | K | L | 611 | |
| 3216 | AAG | GAT | CCC | GAA | TTT | GTA | ATT | CGA | AAG | TAT | GCA | ACC | ATA | CAT | GCA | ACA | AGT | GAC | CGA | GCT | 3275 | |
| 612 | K | D | P | E | F | V | I | R | K | Y | A | T | I | H | A | T | S | D | R | A | 631 | |
| 3276 | ACA | AAA | AAC | TTT | GTT | AGT | GAG | GCG | TTT | TCC | TAT | T | gtaagtttattTTTTcattggaattttttaacaa | | | | | | | 3343 | | |
| 632 | T | K | N | F | V | S | E | A | F | S | Y | F | | | | | | | | 643 | | |
| 3344 | attcttttttag | | TT | GAT | ATG | GTG | CCT | TTT | GAA | AAA | GTC | GTG | CAG | TTA | CTT | TCT | ATG | AAA | ACA | 3405 | | |
| 644 | | | | D | M | V | P | F | E | K | V | V | Q | L | L | S | M | K | T | 659 | | |
| 3406 | TCA | GAT | ACT | TTG | TTT | GTT | GAT | TTT | GTG | GAT | TAT | TGG | ACC | AAA | AGT | TCT | TCT | GAA | ATT | TTT | 3465 | |
| 660 | S | D | T | L | F | V | D | F | V | D | Y | W | T | K | S | S | S | E | I | F | 679 | |
| 3466 | AAA | ATG | CTC | AAG | GAA | CAT | CTC | TCT | GGA | CAC | ATT | GTT | AAG | gtataccaattgttgaattgtaataaca | | | | | | 3532 | | |
| 680 | K | M | L | K | E | H | L | S | G | H | I | V | K | | | | | | | 692 | | |

FIGURE 46 (cont.)

| | | | | | | | | | | | | | | | | | | | | | | |
|------|------------------|--------|-----|-----|------|-----|-----|-----|-----|---|-----|-----|-----|-----|-----|-------------------------|--------------------|-----|-----|------|------|------|
| 3533 | cta | aat | gaa | act | atag | ATA | GGA | AAT | TCT | CAA | TAC | CTT | CAA | AAA | GTT | GGT | ATC | CCT | CAG | GGC | TCA | 3593 |
| 693 | | | | | | I | G | N | S | Q | Y | L | Q | K | V | G | I | P | Q | G | S | 708 |
| 3594 | ATT | CTG | TCA | TCT | TTT | TTG | TGT | CAT | TTC | TAT | ATG | GAA | GAT | TTG | ATT | GAT | GAA | TAC | CTA | TCG | 3653 | |
| 709 | I | L | S | S | F | L | C | H | F | Y | M | E | D | L | I | D | E | Y | L | S | 728 | |
| 3654 | TTT | ACG | AAA | AAG | AAA | GGA | TCA | GTG | TTG | TTA | CGA | GTA | GTC | GAC | GAT | TTC | CTC | TTT | ATA | ACA | 3713 | |
| 729 | F | T | K | K | K | G | S | V | L | L | R | V | V | D | D | F | L | F | I | T | 748 | |
| 3714 | GTT | AAT | AAA | AAG | GAT | GCA | AAA | AAA | TTT | TTG | AAT | TTA | TCT | TTA | AGA | G | gtgagttgctgtcattcc | | | | 3777 | |
| 749 | V | N | K | K | D | A | K | K | F | L | N | L | S | L | R | G | | | | | 764 | |
| 3778 | taagttctaaccg | ttgaag | GA | TTT | GAG | AAA | CAC | AAT | TTT | TCT | ACG | AGC | CTG | GAG | AAA | ACA | GTA | | | | 3840 | |
| 765 | | | | F | E | K | H | N | F | S | T | S | L | E | K | T | V | | | | 778 | |
| 3841 | ATA | AAC | TTT | GAA | AAT | AGT | AAT | GGG | ATA | ATA | AAC | AAT | ACT | TTT | TTT | AAT | GAA | AGC | AAG | AAA | 3900 | |
| 779 | I | N | F | E | N | S | N | G | I | I | N | N | T | F | F | N | E | S | K | K | 798 | |
| 3901 | AGA | ATG | CCA | TTC | TTC | GGT | TTC | TCT | GTG | AAC | ATG | AGG | TCT | CTT | GAT | ACA | TTG | TTA | GCA | TGT | 3960 | |
| 799 | R | M | P | F | F | G | F | S | V | N | M | R | S | L | D | T | L | L | A | C | 818 | |
| 3961 | CCT | AAA | ATT | GAT | GAA | GCC | TTA | TTT | AAC | TCT | ACA | TCT | GTA | GAG | CTG | ACG | AAA | CAT | ATG | GGG | 4020 | |
| 819 | P | K | I | D | E | A | L | F | N | S | T | S | V | E | L | T | K | H | M | G | 838 | |
| 4021 | AAA | TCT | TTT | TTT | TAC | AAA | ATT | CTA | AG | gtatactgtgtaactgaataatagctgacaaataatcag | A | TCG | | | | | | | | 4089 | | |
| 839 | K | S | F | F | Y | K | I | L | R | | | | | | | | | | | S | 848 | |
| 4090 | AGC | CTT | GCA | TCC | TTT | GCA | CAA | GTA | TTT | ATT | GAC | ATT | ACC | CAC | AAT | TCA | AAA | TTC | AAT | TCT | 4149 | |
| 849 | S | L | A | S | F | A | Q | V | F | I | D | I | T | H | N | S | K | F | N | S | 868 | |
| 4150 | TGC | TGC | AAT | ATA | TAT | AGG | CTA | GGA | TAC | TCT | ATG | TGT | ATG | AGA | GCA | CAA | GCA | TAC | TTA | AAA | 4209 | |
| 869 | C | C | N | I | Y | R | L | G | Y | S | M | C | M | R | A | Q | A | Y | L | K | 888 | |
| 4210 | AGG | ATG | AAG | GAT | ATA | TTT | ATT | CCC | CAA | AGA | ATG | TTC | ATA | ACG | G | gtgagtacttatttttaactaga | | | | 4274 | | |
| 889 | R | M | K | D | I | F | I | P | Q | R | M | F | I | T | D | | | | | | 903 | |
| 4275 | aaagtcattaattaac | ccttag | AT | CTT | TTG | AAT | GTT | ATT | GGA | AGA | AAA | ATT | TGG | AAA | AAG | TTG | GCC | | | | 4339 | |
| 904 | | | | L | L | N | V | I | G | R | K | I | W | K | K | L | A | | | | | |

FIGURE 46 (cont.)

4666 gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcggttattagttttgattgacttgtct 4745
4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgccacatgccattaaacgggagtggttaaaca 4825
4826 ttaaaagtaatacatgaggctaatactcctttcatttagaataaggaaagtggttttctataatgaataatgcccgacta 4905
4906 atgcaaaaagacgaagattatcttctaacaagggggattaagcatatccgaaggaaaagagagtaatatcccagtggt 4985
4986 gttgaagaaagcaaggataatttgaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc 5065
5066 cccaggttatccatgggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaataactaatagctcattta 5145
5146 atgtcttatataagggttttgttttttctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttctcaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305
5306 tcctgattttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgc 5385
5386 aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgctggagagtatctccagcggatccttgatgtcaata 5465
5466 acttctattttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc 5544

gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcggttattagttttgattgacttgtct
ttatccttatacttttaagaaagattgacagtggttgctgactactgccacatgccattaaacgggagtggttaaaca
ttaaaagtaatacatgaggctaatactcctttcatttagaataaggaaagtggttttctataatgaataatgcccgacta
atgcaaaaagacgaagattatcttctaacaagggggattaagcatatccgaaggaaaagagagtaatatcccagtggt
gttgaagaaagcaaggataatttgaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc
cccaggttatccatgggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaataactaatagctcattta
atgtcttatataagggttttgttttttctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat
tccgaaatagccaaatttcttggttctcaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc
tcctgattttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgc
aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgctggagagtatctccagcggatccttgatgtcaata
acttctattttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc

FIGURE 47

| | | | | | | | | | | | | | | | | | | | |
|-----------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | | | | | | | | 1 | | | | | | | | | |
| GCCAAGTTCCTGCACTGGCTG | | | | | | | | | | met | ser | val | tyr | val | val | glu | leu | leu | |
| | | | | | | | | | | ATG | AGT | GTG | TAC | GTC | GTC | GAG | CTG | CTC | |
| 10 | | | | | | | | | | 20 | | | | | | | | | |
| arg | ser | phe | phe | tyr | val | thr | glu | thr | thr | phe | gln | lys | asn | arg | | | | | |
| AGG | TCT | TTC | TTT | TAT | GTC | ACG | GAG | ACC | ACG | TTT | CAA | AAG | AAC | AGG | | | | | |
| 30 | | | | | | | | | | | | | | | | | | | |
| leu | phe | phe | tyr | arg | lys | ser | val | trp | ser | lys | leu | gln | ser | ile | | | | | |
| CTC | TTT | TTC | TAC | CGG | AAG | AGT | GTC | TGG | AGC | AAG | TTG | CAA | AGC | ATT | | | | | |
| 40 | | | | | | | | | | 50 | | | | | | | | | |
| gly | ile | arg | gln | his | leu | lys | arg | val | gln | leu | arg | glu | leu | ser | | | | | |
| GGA | ATC | AGA | CAG | CAC | TTG | AAG | AGG | GTG | CAG | CTG | CGG | GAG | CTG | TCG | | | | | |
| 60 | | | | | | | | | | | | | | | | | | | |
| glu | ala | glu | val | arg | gln | his | arg | glu | ala | arg | pro | ala | leu | leu | | | | | |
| GAA | GCA | GAG | GTC | AGG | CAG | CAT | CGG | GAA | GCC | AGG | CCC | GCC | CTG | CTG | | | | | |
| 70 | | | | | | | | | | 80 | | | | | | | | | |
| thr | ser | arg | leu | arg | phe | ile | pro | lys | pro | asp | gly | leu | arg | pro | | | | | |
| ACG | TCC | AGA | CTC | CGC | TTC | ATC | CCC | AAG | CCT | GAC | GGG | CTG | CGG | CCG | | | | | |
| 90 | | | | | | | | | | | | | | | | | | | |
| ile | val | asn | met | asp | tyr | val | val | gly | ala | arg | thr | phe | arg | arg | | | | | |
| ATT | GTG | AAC | ATG | GAC | TAC | GTC | GTG | GGA | GCC | AGA | ACG | TTC | CGC | AGA | | | | | |
| 100 | | | | | | | | | | 110 | | | | | | | | | |
| glu | lys | | ala | glu | arg | leu | thr | ser | arg | val | lys | ala | leu | phe | | | | | |
| GAA | AAG | ARG | GCC | GAG | CGT | CTC | ACC | TCG | AGG | GTG | AAG | GCA | CTG | TTC | | | | | |
| 120 | | | | | | | | | | | | | | | | | | | |
| ser | val | leu | asn | tyr | glu | arg | ala | arg | arg | pro | gly | leu | leu | gly | | | | | |
| AGC | GTG | CTC | AAC | TAC | GAG | CGG | GCG | CGG | CGC | CCC | GGC | CTC | CTG | GGC | | | | | |
| 130 | | | | | | | | | | 140 | | | | | | | | | |
| ala | ser | val | leu | gly | leu | asp | asp | ile | his | arg | ala | trp | arg | thr | | | | | |
| GCC | TCT | GTG | CTG | GGC | CTG | GAC | GAT | ATC | CAC | AGG | GCC | TGG | CGC | ACC | | | | | |
| 150 | | | | | | | | | | | | | | | | | | | |
| phe | val | leu | arg | val | arg | ala | gln | asp | pro | pro | pro | glu | leu | tyr | | | | | |
| TTC | GTG | CTG | CGT | GTG | CGG | GCC | CAG | GAC | CCG | CCG | CCT | GAG | CTG | TAC | | | | | |
| 160 | | | | | | | | | | 170 | | | | | | | | | |
| phe | val | lys | val | asp | val | thr | gly | ala | tyr | asp | thr | ile | pro | gln | | | | | |
| TTT | GTC | AAG | GTG | GAT | GTG | ACG | GGC | GCG | TAC | GAC | ACC | ATC | CCC | CAG | | | | | |
| 180 | | | | | | | | | | | | | | | | | | | |
| asp | arg | leu | thr | glu | val | ile | ala | ser | ile | ile | lys | pro | gln | asn | | | | | |
| GAC | AGG | CTC | ACG | GAG | GTC | ATC | GCC | AGC | ATC | ATC | AAA | CCC | CAG | AAC | | | | | |

FIGURE 47 (cont.)

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 190 | thr | tyr | cys | val | arg | arg | tyr | ala | val | val | 200 | gln | lys | ala | ala | met |
| | ACG | TAC | TGC | GTG | CGT | CGG | TAT | GCC | GTG | GTC | | CAG | AAG | GCC | GCC | ATG |
| | | | | | | | | | | | | | | | | |
| | gly | thr | ser | ala | arg | pro | ser | arg | ala | thr | 210 | ser | tyr | val | gln | cys |
| | GGC | ACG | TCC | GCA | AGG | CCT | TCA | AGA | GCC | ACG | | TCC | TAC | GTC | CAG | TGC |
| | | | | | | | | | | | | | | | | |
| 220 | gln | gly | ile | pro | gln | gly | ser | ile | leu | ser | 230 | thr | leu | leu | cys | ser |
| | CAG | GGG | ATC | CCG | CAG | GGC | TCC | ATC | CTC | TCC | | ACG | CTG | CTC | TGC | AGC |
| | | | | | | | | | | | | | | | | |
| | leu | cys | tyr | gly | asp | met | glu | asn | lys | leu | 240 | phe | ala | gly | ile | arg |
| | CTG | TGC | TAC | GGC | GAC | ATG | GAG | AAC | AAG | CTG | | TTT | GCG | GGG | ATT | CGG |
| | | | | | | | | | | | | | | | | |
| 250 | arg | asp | gly | leu | leu | leu | arg | leu | val | asp | 260 | asp | phe | leu | leu | val |
| | CGG | GAC | GGG | CTG | CTC | CTG | CGT | TTG | GTG | GAT | | GAT | TTC | TTG | TTG | GTG |
| | | | | | | | | | | | | | | | | |
| | thr | pro | his | leu | thr | his | ala | lys | thr | phe | 270 | leu | arg | thr | leu | val |
| | ACA | CCT | CAC | CTC | ACC | CAC | GCG | AAA | ACC | TTC | | CTC | AGG | ACC | CTG | GTC |
| | | | | | | | | | | | | | | | | |
| 280 | arg | gly | val | pro | glu | tyr | gly | cys | val | val | 290 | asn | leu | arg | lys | thr |
| | CGA | GGT | GTC | CCT | GAG | TAT | GGC | TGC | GTG | GTG | | AAC | TTG | CGG | AAG | ACA |
| | | | | | | | | | | | | | | | | |
| | val | val | asn | phe | pro | val | glu | asp | glu | ala | 300 | leu | gly | gly | thr | ala |
| | GTG | GTG | AAC | TTC | CCT | GTA | GAA | GAC | GAG | GCC | | CTG | GGT | GGC | ACG | GCT |
| | | | | | | | | | | | | | | | | |
| 310 | phe | val | gln | met | pro | ala | his | gly | leu | phe | 320 | pro | trp | cys | gly | leu |
| | TTT | GTT | CAG | ATG | CCG | GCC | CAC | GGC | CTA | TTC | | CCC | TGG | TGC | GGC | CTG |
| | | | | | | | | | | | | | | | | |
| | leu | leu | asp | thr | arg | thr | leu | glu | val | gln | 330 | ser | asp | tyr | ser | ser |
| | CTG | CTG | GAT | ACC | CGG | ACC | CTG | GAG | GTG | CAG | | AGC | GAC | TAC | TCC | AGC |
| | | | | | | | | | | | | | | | | |
| 340 | tyr | ala | arg | thr | ser | ile | arg | ala | ser | leu | 350 | thr | phe | asn | arg | gly |
| | TAT | GCC | CGG | ACC | TCC | ATC | AGA | GCC | AGT | CTC | | ACC | TTC | AAC | CGC | GGC |
| | | | | | | | | | | | | | | | | |
| | phe | lys | ala | gly | arg | asn | met | arg | arg | lys | 360 | leu | phe | gly | val | leu |
| | TTC | AAG | GCT | GGG | AGG | AAC | ATG | CGT | CGC | AAA | | CTC | TTT | GGG | GTC | TTG |
| | | | | | | | | | | | | | | | | |
| 370 | arg | leu | lys | cys | his | ser | leu | phe | leu | asp | 380 | leu | gln | val | asn | ser |
| | CGG | CTG | AAG | TGT | CAC | AGC | CTG | TTT | CTG | GAT | | TTG | CAG | GTG | AAC | AGC |

FIGURE 47 (cont.)

390
 leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
 CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

 400 410
 ala tyr arg phe his ala cys val leu gln leu pro phe his gln
 GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

 420
 gln val trp lys asn pro his phe ser cys ala ser ser leu thr
 CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

 430 440
 arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
 CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

 450
 val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
 GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

 460 470
 arg ala val ala val pro pro ser ile pro ala gln ala asp ser
 CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

 480
 thr pro cys his leu arg ala thr pro gly val thr gln asp ser
 ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

 490 500
 pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
 CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

 510
 pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
 CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

 520 530
 his pro gly leu met ala thr arg pro gln pro gly arg glu gln
 CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

 540
 thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
 ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGC

 550 560
 arg gly gly pro his pro gly leu his arg trp glu ser glu ala
 AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

 564
 OP
 TGA GTGAGTGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

 CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

AGGCTGGCGTTTCGGTCCACCCCAGGGCCAGCTTTTTCCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCATTGTTTACCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT
TTTCAGTTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

[illegible]

FIGURE 48

| | |
|-----------|--|
| Motif -1 | |
| Ep p123 | ...LVVSLIRCFFYVTEQQKSYSKT... |
| Sp Tez1 | ...FIIPILQSFFYITESSDLRNRT... |
| Sc Est2 | ...LIPKIIQTFFYCTEISSTVTIV... |
| Hs TCP1 | ...YVVELLRSFFYVTETTFQKNRL... |
| consensus | FFY TE |
| Motif 0 | K |
| | p hhh K hR h R |
| Ep p123 | ...KSLGFAPGKLRLLPKKT--TFRPIMTFNKKIV... |
| Sp Tez1 | ...QKTTLPPAVIRLLPKKN--TFRLITNLRKRFL... |
| Sc Est2 | ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD... |
| Hs TCP1 | ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG... |
| consensus | R PK R I |
| Motif A | AF |
| | h hDh GY h |
| Ep p123 | ...PKLFFATMDIEKCYDSVNREKLSTFLK... |
| Sp Tez1 | ...RKKYFVRIDIKSCYDRIKQDLMFRIVK... |
| Sc Est2 | ...PELYFMKFDVKSCYDSIPRMECMRILK... |
| Hs TCP1 | ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//... |
| consensus | F D YD |
| Motif B | hPQG pS hh |
| Ep p123 | ...NGKFYKQTKGIPQGLCVSSILSSFYYA... |
| Sp Tez1 | ...GNSQYLQKVGIPQGSILSSFLCHFYME... |
| Sc Est2 | ...EDKCYIREDGLFQGSSLSAPIVDLVYD... |
| Hs TCP1 | ...RATSYVQCQGIPQGSILSTLLCSLCYG... |
| consensus | G QG S |
| Motif C | Y |
| | h F DDhhh |
| Ep p123 | ...PNVNLLMRLTDDYLLITTQENN... |
| Sp Tez1 | ...KKGSVLLRVVDDFLFITVNKKD... |
| Sc Est2 | ...SQDTLILKLADDFLIISTDQQQ... |
| Hs TCP1 | ...RRDGLLLRLVDDFLLVTPHLTH... |
| consensus | DD L |
| Motif D | Gh h cK |
| Ep p123 | ...NVSRENGFKFNMKKL... |
| Sp Tez1 | ...LNLSLRGFEEKHNFST... |
| Sc Est2 | ...KKLAMGGFQKYNAKA... |
| Hs TCP1 | ...LRTLVRGVPEYGCVV... |
| consensus | G |

FIGURE 49

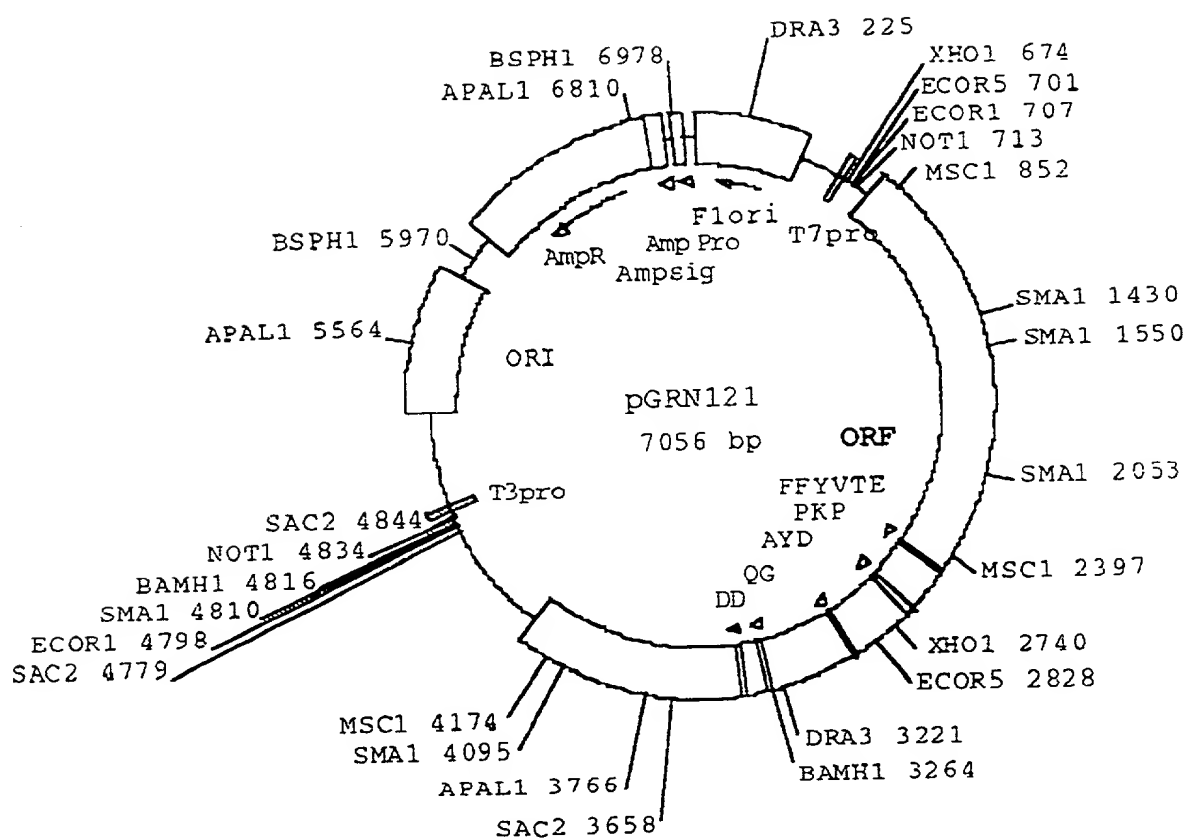


FIGURE 50

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
 51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GCGCCTGGG
 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
 251 CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCG CGAGGCCTTC
 401 ACCACCAGCG TGCAGAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
 501 TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT GGNTCCACG
 551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
 601 TCAGGCCCGG CCCCCGCCAC ACGTANTGG ACCCGAANGC GTCTGGGATC
 651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701 CCAGCCCCCG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
 751 GTTGCCCAAG AGGCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801 CCGTTGGGCA GGGGTCCTGG GCCACCCCG GCAGGACGCC TGGACCGAGT
 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG
 951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
 1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCTCTAC
 1051 TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCTACTC AATATATCTG
 1101 AGGCCCAGCC TGAAGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
 1151 TTCCAGGCCT TGGATGCCAG GATTCCCCCG AGGTTGCCCC GCCTGCCCCA
 1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAACCACG
 1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
 1301 GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
 1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG
 1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
 1451 CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TCGGGGACTG
 1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
 1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
 1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
 1801 TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
 1851 CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
 1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
 1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCAGCG TGCTCAACTA
 2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
 2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG
 2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
 2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
 2251 AACCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC

FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
 2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
 2401 GCGCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
 2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
 2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
 2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
 2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGC GTTTGGT
 2651 GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
 2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACCTG
 2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC
 2801 GGCTTTTGTG CAGATGCCGG CCCACGGCCT ATTCCCCTGG TCGGGCCTGC
 2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
 2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG
 2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTGACA
 3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
 3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
 3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGA GAACCCACACA TTTTTCCTGC
 3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
 3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC
 3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC
 3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG
 3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
 3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT
 3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
 3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC
 3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
 3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
 3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG
 3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA
 3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
 3801 GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA
 3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
 3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
 3951 GGGGGGAGGT GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT
 4001 TTGAAAAAAAA AAAAAAAAAA AAAAAAAAAA

FIGURE 51

GCAGCGCTGCGTCTCTGCGCAGGTGGGAAGCCCTGGCCCCCGCCACCCCGCGATGCC
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
CCTCCCGACGACGAGGACGACGCTGCAACCTTGGGACCGGGGCCGCTGGGGGCGCTACGG

a A A I R P A A H V G S P C F G H F R D A -
b Q R C V L L R T W E A L A P A T P A M P -
c S A A S C C A R G K P W F R P P F R C R -

CCGCGCTCCCGGCTGCGGAGCGGTGGGCTCCTGCTGCGCAGCCACTACCGGAGGTGCT
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
CGC3CGAGGGGGGACG3CTCGGCACGCGAGGGACGACGCGTGGGTGATGGCGCTCCACGA

a A R S P L I S R A L P A A Q P I P R G A -
b R A P R C K A V R E L L R S H Y R E V L -
c A L P A A E P C A P C C A A T T A R C C -

GC0GCTGGCCAGTTCTGTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGCG
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
CGCGACCGGTGCAAGCAGCGCGCGGACCCCGGGTCCCGACCGCCGACCACGTGCGGCT

a A A G H V R A A P G A P G I A A G A A R -
b P L A T F V R R L G P Q G W R L V Q R G -
c R W P R S C G A W G P R A G G W C S A G -

GGACCCGGCGCTTTCCGCGCGNTGGTGGCCCCANTGCGTGGTGGCGTCCCTGGGANGN
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
CCTGGGCCGCGAAGGCGCGCNACCACCGGGTNACGNACCACACGACGCGCACCGCTNCGN

a G P G G F P R ? G G P ? ? G V R A L G ? -
b D P A A F R A ? V A ? C ? V C V P W ? ? -
c T R R L S A R W W P ? A W C A C T G ? ? -

ANGGNGCGCCCCCGCGCCCCCTCCTTCGCGCAGGTGTCTGCTGAANGANCTGGTGCG
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
TNCGNGCGCGCGCGCGCGGGGAGGAAGGCGGTCCACAGGACGGACTTNCINGACCCG

a ? A A F R R P L L P P G V L P E ? ? G G -
b ? ? P P A A P S F R Q V S C L ? ? L V A -
c G ? P P P P P P S A R C P A ? ? ? W W P -

CGGAGTGCTGCANANGCTGTGCGANCCCCCGCGAANAACGTGCTGGGCTTCG3CTTG3C
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
GGCTCACGAGTNTNTGACACGCTNGCGCGCGCTTNTTGCACGACUGGAAGUGGAAGCG

a P S A A ? A V R ? R R E ? R A G L R L R -
b R V L ? ? L C ? R G A ? N V L A F C P A -
c E C C ? ? C A ? A A R ? T C W P S A S R -

GCTGCTGGACGGGGCCCGGGGGCCCCCGAGCCCTTCACCACCAGGCTGGCAGCTA
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
CGACGACCTGCCCCGGGGGCCCCCGGGGGGCTTCGGAAGTGGTGGTGGCACCGGTGGT

a A A G R G P R G P P R G L H H Q R A Q L -
b L L D G A R G G F P E A F T T S V R S Y
c C W T G P A G A F F R F S P P A C A A T -

| Year | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | |

A P A Q H G D R R T A G E F G V G A A A A
 B L P N T V T D A L R G S G A W G L L L K -
 C C P T R * F T H C G C A G K G G C C C A -

A P R C R R R A G S P A G T L R ? ? C A G -
 B R V G D D V L V H L L A R C A ? F V L V -
 C A W A T T C W F T C W H A A R ? L C W W .

G S Q L R L P ? V R A A A V P A R R C ? -
 P P S C A Y ? V C G P P L Y Q L G A A T -
 F A A P T ? C A G R R C T S S A L L L -

L S C P A P A T R ? W T R ? R L G S N G P -
 b U A R F P F H A ? G P E ? V W D F T G L -
 c R P G P R H T L ? D F ? A S G I O R A W

G T I A S C K P C S P W A A S P G C E E -
 E P * R Q G G R C P P G L P A F G A R R -
 N H S V R E A G V P L G C O P R V R G G -

A R G Q C Q P K S A V A Q E A Q A W R C
D R G G S A S R S L P L P K R P R R G A A
F A G A V F A E V C R C F R G F G V A L P -

A P - A C A D A R W A C V L G F F G Q D A -
 B F E F E R T P V G Q G S W A H F G R T P -
 C L E R S G R P L G R G P G P T R A C E L -

[illegible]

TGGACCGAGTACCGTGGTTTCTGTGTGGTGTACCTCCACACCCGCCCAAGAAGCCAC
 F41 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
 ACCTGGCTCACTGGCACCAAGACACACACAGTGGACGGTCTGGGGGGCTTTTTCGGCTC
 W T E * P W F L C G V T C Q T R R R S H -
 G P S D R G F C V V S P A R F A E E A T
 D P V T V V S V W C H L P D P P K K P F -
 CTCCTTGGAGGGTGGCTCTCTGGCACGGCCACTCCACCCATCCGTGGGGCGCCAGCA
 901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
 CAGAAACCTCCACCGCGAGAGACCGTGGCGGGTGAGGGTGGGTAGGCACCCGCGCGTCTGT
 L P C G C A L W H A F L P P T R G F F A
 S L E G A L S C T R H S H P S V G R Q H -
 L W R V R S L A R A T P T H P W A A S T -
 CCAAGCGGGGCCCCCATCCACATCGCGGCCACCAAGTCTTGGGACACGCCCTTGTCCCCCG
 961 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
 GGTGCGCCCGGGGGGTAGGTGTAGCGCGGGTGTTGCAAGAACCTGTGCGGAACAGGGGCG
 P K C P P I H I A A T T S W D T F C P P
 H A G P P S T S R P P R P G T R L V P P
 T R A F H P H R G H H V L G H A L S P G -
 GTGTACGCGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGNACACTGGNCCCTT
 1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
 CATATGCGCTCTGGTTCGTGAAGGAGATGAGGAGTCCGCTGTTCTNTGTGACGCGNCGGAG
 V Y A E T K H F L Y S S C D K ? T A ? L -
 C T P R P S T S S T P Q A T ? T L R P S -
 V R R D G A L P L L L R R Q ? H C ? P P -
 CTTCCTACTCAATATATCTGAGGCCAGCCTGACTGCGGTTCGGGAGGTTCTGTGGAGATCA
 1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
 GAAGGATGAGTTATATAGACTCCGGGTCCGACTGACCGCAAGCCCTCCAAAGCACCTCTCTT
 L P T Q Y I * G P A * L A F G R F V E T
 F L L N I S E A Q P D W R S G G S W R ? -
 S Y S I Y L R P S L T G V R E V R G D ? -
 NTCTTTCTGGTTCAGGGCCTTGGATGCCAGGATTCCCGGCAGGTTGGCCCGGCTGCCCA
 1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
 NAGAAAGACCAAGGTTCGGAACCTTACGGTCTTAAAGGGGGTTCACACGGGGCGGACGGGT
 P F L V P G L G C Q D S P Q V A P P A P -
 S F W F Q A L D A R I P R R L P R L P Q -
 L S G F R P W M P G F P A G C P A C F S -
 GCGNTACTGGCAATGCGGCCCTCTTTCTGGAGCTCTCTTGGGAACCAAGCGCAGTGGCC
 1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
 CGCNATGACCGTTTACGCGGGGACAAAGACTTCGAGCAACCTTGGTGGCGGTACAGGG
 A ? L A N A A P V S G A A W E P R A V F -
 R Y W Q M R F L F L E L L G N H A Q C P -
 ? T G K C G P C F W S C L G T T R S A F -

[illegible][illegible]

A S C T G ' ' V C T S S S C S C L S F M S -
 B F A L A D E C V R R R A A Q V F L L C H -
 C L H W L M S V Y V V E L L R S F F Y V T -

```

      R R P P F K R T G S F S T G R V S G A S -
b      C D H V F K E Q A L F L P E E C L E Q V -
c      E T T F Q K N R L F F Y R K S V W S K L

```

A C K A L E S D S T * R G C S C G S C R K
 B A K H W N Q T A L E E C A A A C A V C S -
 C Q S T G T R Q H L K R V Q L R E I S E A -

A Q R S L S I G K P G P P C * R F D S A E -
B E G Q A A S C S Q A R P A D V O T P L H -
C E V R Q H R E A R P A L L T S R L R F I

S P E L T G C G R L * T W T T S W E P E -
P Q A * R A A A D C E H G L R R G S Q N
P K P D G L R P I V N M D Y V V G A R T

R S A E K R C P S V S P H G * R H C S A -
V P Q R K E G R A S H L E C E G T V Q R -
F R R E K R A E R L T S R V K A L F S V -

C S T T S G R G A P A S W A P L C W A W -
A O L R A G A A P R P P G R I C A G P G -
L N Y E R A R R P G L L G A E V L G I D -

[illegible]

[illegible][illegible]

[illegible]

a A T T P A M P G P P S E P V S P S T A A -
b R L L Q L C F D L H Q C Q S H L Q F R L -
c D Y S S Y A R T S I R A S L T E N R G F

[illegible]

H S F L G G T C V A N S L G S C G * S V T
 L Q G W E E H A S Q T L W G L A A E V S Q
 C K A G R N M R R K L F G V L R L K C H S

a A C F W I C R T A S R R C A F I S T R -
b P V S G F A G E Q F P D G V H Q H L Q D -
c L F L D L Q V N S L Q T V C T N I Y K I -

a S S C C R R T G F T H V C C E S H F I S -
b T T A A G V Q V S R M C A A A P I S S A -
c L L L Q A Y R F H A C V L O L P F H O O -

A K F G R T P H F S C A S S L T R P F S A -
 B S L E E P H I F P A R H L * H G L P L L
 C V W K N P T F F L R V I S D T A S L C Y

T P S * K F R T Q G C E W G P R A F P A -
 L H F E S Q E R P D V A G G Q G R R R P
 S I L K A K N A C M S L C A K C A A C P -

L C P P P P C S G C A T E H S C S S * L -
 S A I R G R A V A V P P S I P A Q A D S -
 L P S E A V Q W L C H Q A F L L K L T R -

A D T V S P T C H S W G H S G Q F R R S * -
b T P C H L R A T P G V T Q D S P D A A E -
c H R V T Y V F L L G S L R T A Q T Q L S -

[illegible]

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[illegible]

A F A I V H P S P C P P L P S T P T I Q V -
 B S E L F T P E P A L L C L P F F F S R W -
 C P H C S P L A L P S F A F H P H H P G S -

5 F T L E R T L G A L G I W S D Q R E A L -
 6 F F * E G P W E L W E F G V T K G V P C -
 7 D E E F D T G S S C N L E * P K V C F V -

A Y T G F D P A P G W G S I W V K L G G C
B T Q A R T L H L D G G P C G S N W G E V
C H R R C P C T W M C V P V G O I G G E C

```

A   A V G V K Y * I Y E F F S F E K K K K K
B   L W E * N T E Y M S F S V L K K K K K K
C   C G S K I L N I * V F Q F * K K K K K K

```

| | | | | | |
|---|---|---|---|---|---|
| a | K | K | K | - | |
| b | | K | K | - | |
| c | | | K | K | - |

FIGURE 52

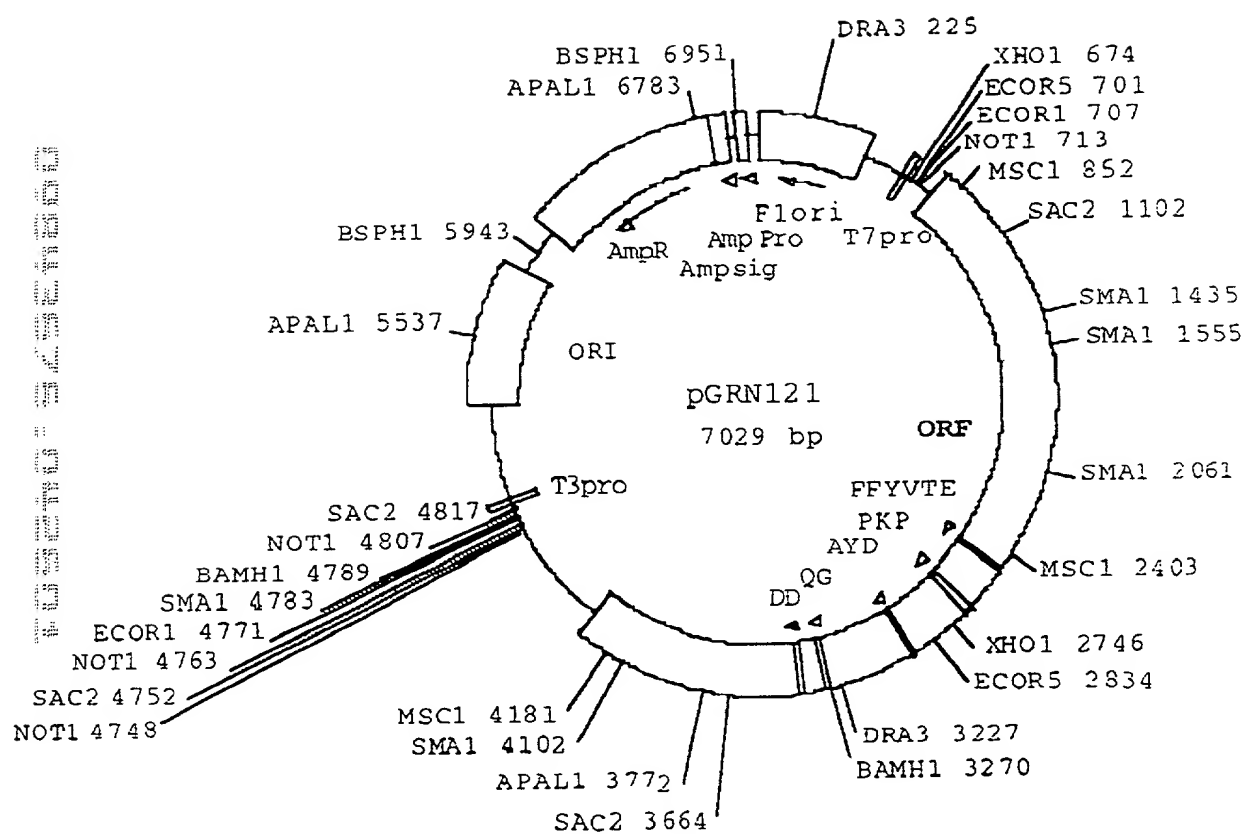


FIGURE 53

1
 met
 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG
 10
 pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC
 20 30
 his tyr arg glu val leu pro leu ala thr phe val arg arg leu
 CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG
 40
 gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
 GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT
 50 60
 phe arg ala leu val ala gln cys leu val cys val pro trp asp
 TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC
 70
 ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
 GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC
 80 90
 leu lys glu leu val ala arg val leu gln arg leu cys glu arg
 CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC
 100
 gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
 GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG
 110 120
 ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
 GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC
 130
 tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
 TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | | | | | | | | | 140 | | | 150 | | |
| trp | gly | leu | leu | leu | arg | arg | val | gly | asp | asp | val | leu | val | his | | | |
| TGG | GGG | CTG | CTG | CTG | CGC | CGC | GTG | GGC | GAC | GAC | GTG | CTG | GTT | CAC | | | |
| | | | | | | | | | | | | 160 | | | | | |
| leu | leu | ala | arg | cys | ala | leu | phe | val | leu | val | ala | pro | ser | cys | | | |
| CTG | CTG | GCA | CGC | TGC | GCG | CTC | TTT | GTG | CTG | GTG | GCT | CCC | AGC | TGC | | | |
| | | | | | | | | | | | | 170 | | | 180 | | |
| ala | tyr | gln | val | cys | gly | pro | pro | leu | tyr | gln | leu | gly | ala | ala | | | |
| GCC | TAC | CAG | GTG | TGC | GGG | CCG | CCG | CTG | TAC | CAG | CTC | GGC | GCT | GCC | | | |
| | | | | | | | | | | | | 190 | | | | | |
| thr | gln | ala | arg | pro | pro | pro | his | ala | ser | gly | pro | arg | arg | arg | | | |
| ACT | CAG | GCC | CGG | CCC | CCG | CCA | CAC | GCT | AGT | GGA | CCC | CGA | AGG | CGT | | | |
| | | | | | | | | | | | | 200 | | | 210 | | |
| leu | gly | cys | glu | arg | ala | trp | asn | his | ser | val | arg | glu | ala | gly | | | |
| CTG | GGA | TGC | GAA | CGG | GCC | TGG | AAC | CAT | AGC | GTC | AGG | GAG | GCC | GGG | | | |
| | | | | | | | | | | | | 220 | | | | | |
| val | pro | leu | gly | leu | pro | ala | pro | gly | ala | arg | arg | arg | gly | gly | | | |
| GTC | CCC | CTG | GGC | CTG | CCA | GCC | CCG | GGT | CCG | AGG | AGG | CGC | GGG | GGC | | | |
| | | | | | | | | | | | | 230 | | | 240 | | |
| ser | ala | ser | arg | ser | leu | pro | leu | pro | lys | arg | pro | arg | arg | gly | | | |
| AGT | GCC | AGC | CGA | AGT | CTG | CCG | TTG | CCC | AAG | AGG | CCC | AGG | CGT | GGC | | | |
| | | | | | | | | | | | | 250 | | | | | |
| ala | ala | pro | glu | pro | glu | arg | thr | pro | val | gly | gln | gly | ser | trp | | | |
| GCT | GCC | CCT | GAG | CCG | GAG | CGG | ACG | CCC | GTT | GGG | CAG | GGG | TCC | TGG | | | |
| | | | | | | | | | | | | 260 | | | 270 | | |
| ala | his | pro | gly | arg | thr | arg | gly | pro | ser | asp | arg | gly | phe | cys | | | |
| GCC | CAC | CCG | GGC | AGG | ACG | CGT | GGA | CCG | AGT | GAC | CGT | GGT | TTC | TGT | | | |
| | | | | | | | | | | | | 280 | | | | | |
| val | val | ser | pro | ala | arg | pro | ala | glu | glu | ala | thr | ser | leu | glu | | | |
| GTG | GTG | TCA | CCT | GCC | AGA | CCC | GCC | GAA | GAA | GCC | ACC | TCT | TTG | GAG | | | |

[illegible]

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 290 | | | | | | | | | | | | | 300 | |
| gly | ala | leu | ser | gly | thr | arg | his | ser | his | pro | ser | val | gly | arg |
| GGT | GCG | CTC | TCT | GGC | ACG | CGC | CAC | TCC | CAC | CCA | TCC | GTG | GGC | CGC |
| 310 | | | | | | | | | | | | | | |
| gln | his | his | ala | gly | pro | pro | ser | thr | ser | arg | pro | pro | arg | pro |
| CAG | CAC | CAC | GCG | GGC | CCC | CCA | TCC | ACA | TCG | CGG | CCA | CCA | CGT | CCC |
| 320 | | | | | | | | | | | | | 330 | |
| trp | asp | thr | pro | cys | pro | pro | val | tyr | ala | glu | thr | lys | his | phe |
| TGG | GAC | ACG | CCT | TGT | CCC | CCG | GTG | TAC | GCC | GAG | ACC | AAG | CAC | TTC |
| 340 | | | | | | | | | | | | | | |
| leu | tyr | ser | ser | gly | asp | lys | glu | gln | leu | arg | pro | ser | phe | leu |
| CTC | TAC | TCC | TCA | GGC | GAC | AAG | GAG | CAG | CTG | CGG | CCC | TCC | TTC | CTA |
| 350 | | | | | | | | | | | | | 360 | |
| leu | ser | ser | leu | arg | pro | ser | leu | thr | gly | ala | arg | arg | leu | val |
| CTC | AGC | TCT | CTG | AGG | CCC | AGC | CTG | ACT | GGC | GCT | CGG | AGG | CTC | GTG |
| 370 | | | | | | | | | | | | | | |
| glu | thr | ile | phe | leu | gly | ser | arg | pro | trp | met | pro | gly | thr | pro |
| GAG | ACC | ATC | TTT | CTG | GGT | TCC | AGG | CCC | TGG | ATG | CCA | GGG | ACT | CCC |
| 380 | | | | | | | | | | | | | 390 | |
| arg | arg | leu | pro | arg | leu | pro | gln | arg | tyr | trp | gln | met | arg | pro |
| CGC | AGG | TTG | CCC | CGC | CTG | CCC | CAG | CGC | TAC | TGG | CAA | ATG | CGG | CCC |
| 400 | | | | | | | | | | | | | | |
| leu | phe | leu | glu | leu | leu | gly | asn | his | ala | gln | cys | pro | tyr | gly |
| CTG | TTT | CTG | GAG | CTG | CTT | GGG | AAC | CAC | GCG | CAG | TGC | CCC | TAC | GGG |
| 410 | | | | | | | | | | | | | 420 | |
| val | leu | leu | lys | thr | his | cys | pro | leu | arg | ala | ala | val | thr | pro |
| GTG | CTC | CTC | AAG | ACG | CAC | TGC | CCG | CTG | CGA | GCT | GCG | GTC | ACC | CCA |
| 430 | | | | | | | | | | | | | | |
| ala | ala | gly | val | cys | ala | arg | glu | lys | pro | gln | gly | ser | val | ala |
| GCA | GCC | GGT | GTC | TGT | GCC | CGG | GAG | AAG | CCC | CAG | GGC | TCT | GTG | GCG |

FIGURE 53 (cont.)

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 440 | | | | | | | | | | | | | | 450 | |
| ala | pro | glu | glu | glu | asp | thr | asp | pro | arg | arg | leu | val | gln | leu | |
| GCC | CCC | GAG | GAG | GAG | GAC | ACA | GAC | CCC | CGT | CGC | CTG | GTG | CAG | CTG | |
| 460 | | | | | | | | | | | | | | | |
| leu | arg | gln | his | ser | ser | pro | trp | gln | val | tyr | gly | phe | val | arg | |
| CTC | CGC | CAG | CAC | AGC | AGC | CCC | TGG | CAG | GTG | TAC | CGC | TTC | GTG | CGG | |
| 470 | | | | | | | | | | | | | | 480 | |
| ala | cys | leu | arg | arg | leu | val | pro | pro | gly | leu | trp | gly | ser | arg | |
| GCC | TGC | CTG | CGC | CGG | CTG | GTG | CCC | CCA | GGC | CTC | TGG | GGC | TCC | AGG | |
| 490 | | | | | | | | | | | | | | | |
| his | asn | glu | arg | arg | phe | leu | arg | asn | thr | lys | lys | phe | ile | ser | |
| CAC | AAC | GAA | CGC | CGC | TTC | CTC | AGG | AAC | ACC | AAG | AAG | TTC | ATC | TCC | |
| 500 | | | | | | | | | | | | | | 510 | |
| leu | gly | lys | his | ala | lys | leu | ser | leu | gln | glu | leu | thr | trp | lys | |
| CTG | GGG | AAG | CAT | GCC | AAG | CTC | TCG | CTG | CAG | GAG | CTG | ACG | TGG | AAG | |
| 520 | | | | | | | | | | | | | | | |
| met | ser | val | arg | asp | cys | ala | trp | leu | arg | arg | ser | pro | gly | val | |
| ATG | AGC | GTG | CGG | GAC | TGC | GCT | TGG | CTG | CGC | AGG | AGC | CCA | GGG | GTT | |
| 530 | | | | | | | | | | | | | | 540 | |
| gly | cys | val | pro | ala | ala | glu | his | arg | leu | arg | glu | glu | ile | leu | |
| GGC | TGT | GTT | CCG | GCC | GCA | GAG | CAC | CGT | CTG | CGT | GAG | GAG | ATC | CTG | |
| 550 | | | | | | | | | | | | | | | |
| ala | lys | phe | leu | his | trp | leu | met | ser | val | tyr | val | val | glu | leu | |
| GCC | AAG | TTC | CTG | CAC | TGG | CTG | ATG | AGT | GTG | TAC | GTC | GTC | GAG | CTG | |
| 560 | | | | | | | | | | | | | | 570 | |
| leu | arg | ser | phe | phe | tyr | val | thr | glu | thr | thr | phe | gln | lys | asn | |
| CTC | AGG | TCT | TTC | TTT | TAT | GTC | ACG | GAG | ACC | ACG | TTT | CAA | AAG | AAC | |
| 580 | | | | | | | | | | | | | | | |
| arg | leu | phe | phe | tyr | arg | pro | ser | val | trp | ser | lys | leu | gln | ser | |
| AGG | CTC | TTT | TTC | TAC | CGG | CCG | AGT | GTC | TGG | AGC | AAG | TTG | CAA | AGC | |
| 590 | | | | | | | | | | | | | | 600 | |
| ile | gly | ile | arg | gln | his | leu | lys | arg | val | gln | leu | arg | glu | leu | |
| ATT | GGA | ATC | AGA | CAG | CAC | TTG | AAG | AGG | GTG | CAG | CTG | CGG | GAG | CTG | |

FIGURE 53 (cont.)

610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

630
640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

660
670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

690
700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

720
730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

750
760
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

FIGURE 53 (cont.)

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | 770 | | | | | | | | | | | 780 |
| thr | asp | leu | gln | pro | tyr | met | arg | gln | phe | val | ala | his | leu | gln |
| ACA | GAC | CTC | CAG | CCG | TAC | ATG | CGA | CAG | TTC | GTG | GCT | CAC | CTG | CAG |
| | | | | | | | | 790 | | | | | | |
| glu | thr | ser | pro | leu | arg | asp | ala | val | val | ile | glu | gln | ser | ser |
| GAG | ACC | AGC | CCG | CTG | AGG | GAT | GCC | GTC | GTC | ATC | GAG | CAG | AGC | TCC |
| | | | | | | | | | | | | | | |
| | | | 800 | | | | | | | | | | | 810 |
| ser | leu | asn | glu | ala | ser | ser | gly | leu | phe | asp | val | phe | leu | arg |
| TCC | CTG | AAT | GAG | GCC | AGC | AGT | GGC | CTC | TTC | GAC | GTC | TTC | CTA | CGC |
| | | | | | | | | | | | | | | |
| | | | | | | | | 820 | | | | | | |
| phe | met | cys | his | his | ala | val | arg | ile | arg | gly | lys | ser | tyr | val |
| TTC | ATG | TGC | CAC | CAC | GCC | GTG | CGC | ATC | AGG | GGC | AAG | TCC | TAC | GTC |
| | | | | | | | | | | | | | | |
| | | | 830 | | | | | | | | | | | 840 |
| gln | cys | gln | gly | ile | pro | gln | gly | ser | ile | leu | ser | thr | leu | leu |
| CAG | TGC | CAG | GGG | ATC | CCG | CAG | GGC | TCC | ATC | CTC | TCC | ACG | CTG | CTC |
| | | | | | | | | | | | | | | |
| | | | | | | | | 850 | | | | | | |
| cys | ser | leu | cys | tyr | gly | asp | met | glu | asn | lys | leu | phe | ala | gly |
| TGC | AGC | CTG | TGC | TAC | GGC | GAC | ATG | GAG | AAC | AAG | CTG | TTT | GCG | GGG |
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| | | | 860 | | | | | | | | | | | 870 |
| ile | arg | arg | asp | gly | leu | leu | leu | arg | leu | val | asp | asp | phe | leu |
| ATT | CGG | CGG | GAC | GGG | CTG | CTC | CTG | CGT | TTG | GTG | GAT | GAT | TTC | TTG |
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| | | | | | | | | 880 | | | | | | |
| leu | val | thr | pro | his | leu | thr | his | ala | lys | thr | phe | leu | arg | thr |
| TTG | GTG | ACA | CCT | CAC | CTC | ACC | CAC | GCG | AAA | ACC | TTC | CTC | AGG | ACC |
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| | | | 890 | | | | | | | | | | | 900 |
| leu | val | arg | gly | val | pro | glu | tyr | gly | cys | val | val | asn | leu | arg |
| CTG | GTC | CGA | GGT | GTC | CCT | GAG | TAT | GGC | TGC | GTG | GTG | AAC | TTG | CGG |
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| | | | | | | | | 910 | | | | | | |
| lys | thr | val | val | asn | phe | pro | val | glu | asp | glu | ala | leu | gly | gly |
| AAG | ACA | GTG | GTG | AAC | TTC | CCT | GTA | GAA | GAC | GAG | GCC | CTG | GGT | GGC |
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| | | | 920 | | | | | | | | | | | 930 |
| thr | ala | phe | val | gln | met | pro | ala | his | gly | leu | phe | pro | trp | cys |
| ACG | GCT | TTT | GTT | CAG | ATG | CCG | GCC | CAC | GGC | CTA | TTC | CCC | TGG | TGC |

FIGURE 53 (cont.)

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|--|------|--|--|
| | | | | | | | | | | | | | 940 | | | | | |
| gly | leu | leu | leu | asp | thr | arg | thr | leu | glu | val | gln | ser | asp | tyr | | | | |
| GGC | CTG | CTG | CTG | GAT | ACC | CGG | ACC | CTG | GAG | GTG | CAG | AGC | GAC | TAC | | | | |
| | | | | | | | | | | | | | 950 | | | 960 | | |
| ser | ser | tyr | ala | arg | thr | ser | ile | arg | ala | ser | val | thr | phe | asn | | | | |
| TCC | AGC | TAT | GCC | CGG | ACC | TCC | ATC | AGA | GCC | AGT | GTC | ACC | TTC | AAC | | | | |
| | | | | | | | | | | | | | 970 | | | | | |
| arg | gly | phe | lys | ala | gly | arg | asn | met | arg | arg | lys | leu | phe | gly | | | | |
| CGC | GGC | TTC | AAG | GCT | GGG | AGG | AAC | ATG | CGT | CGC | AAA | CTC | TTT | GGG | | | | |
| | | | | | | | | | | | | | 980 | | | 990 | | |
| val | leu | arg | leu | lys | cys | his | ser | leu | phe | leu | asp | leu | gln | val | | | | |
| GTC | TTG | CGG | CTG | AAG | TGT | CAC | AGC | CTG | TTT | CTG | GAT | TTG | CAG | GTG | | | | |
| | | | | | | | | | | | | | 1000 | | | | | |
| asn | ser | leu | gln | thr | val | cys | thr | asn | ile | tyr | lys | ile | leu | leu | | | | |
| AAC | AGC | CTC | CAG | ACG | GTG | TGC | ACC | AAC | ATC | TAC | AAG | ATC | CTC | CTG | | | | |
| | | | | | | | | | | | | | 1010 | | | 1020 | | |
| leu | gln | ala | tyr | arg | phe | his | ala | cys | val | leu | gln | leu | pro | phe | | | | |
| CTG | CAG | GCG | TAC | AGG | TTT | CAC | GCA | TGT | GTG | CTG | CAG | CTC | CCA | TTT | | | | |
| | | | | | | | | | | | | | 1030 | | | | | |
| his | gln | gln | val | trp | lys | asn | pro | thr | phe | phe | leu | arg | val | ile | | | | |
| CAT | CAG | CAA | GTT | TGG | AAG | AAC | CCC | ACA | TTT | TTC | CTG | CGC | GTC | ATC | | | | |
| | | | | | | | | | | | | | 1040 | | | 1050 | | |
| ser | asp | thr | ala | ser | leu | cys | tyr | ser | ile | leu | lys | ala | lys | asn | | | | |
| TCT | GAC | ACG | GCC | TCC | CTC | TGC | TAC | TCC | ATC | CTG | AAA | GCC | AAG | AAC | | | | |
| | | | | | | | | | | | | | 1060 | | | | | |
| ala | gly | met | ser | leu | gly | ala | lys | gly | ala | ala | gly | pro | leu | pro | | | | |
| GCA | GGG | ATG | TCG | CTG | GGG | GCC | AAG | GGC | GCC | GCC | GGC | CCT | CTG | CCC | | | | |
| | | | | | | | | | | | | | 1070 | | | 1080 | | |
| ser | glu | ala | val | gln | trp | leu | cys | his | gln | ala | phe | leu | leu | lys | | | | |
| TCC | GAG | GCC | GTG | CAG | TGG | CTG | TGC | CAC | CAA | GCA | TTC | CTG | CTC | AAG | | | | |
| | | | | | | | | | | | | | 1090 | | | | | |
| leu | thr | arg | his | arg | val | thr | tyr | val | pro | leu | leu | gly | ser | leu | | | | |
| CTG | ACT | CGA | CAC | CGT | GTC | ACC | TAC | GTG | CCA | CTC | CTG | GGG | TCA | CTC | | | | |

FIGURE 53 (cont.)

1100 1110
 arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
 AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG
 1120
 leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
 CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC
 1130 1132
 phe lys thr ile leu asp OP
 TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA
 CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCCACACCC
 AGGCCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC
 GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC
 CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG
 CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
 CGCCATTGTTCACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA
 GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA
 CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC
 TGTGGGAGTAAAATACTGAATATATGAGTTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

FIGURE 54

KPN1 17050
KPN1 18560
ECOR1 19475
SAC1 19652
SAC1 21083
ECOR1 23539
SAC1 24607
SAC1 29043

<-TCP